

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION  
International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 :  C12Q 1/68, C12P 19/34, C12N 15/63, 15/85, 15/11, C07H 21/04, A61K 48/00		A1	(11) International Publication Number: <b>WO 99/09214</b>  (43) International Publication Date: 25 February 1999 (25.02.99)
(21) International Application Number: PCT/US98/16488		(74) Agents: LICATA, Jane, Massey et al.; Law Offices of Jane Massey Licata, 66 E. Main Street, Marlton, NJ 08053 (US).	
(22) International Filing Date: 7 August 1998 (07.08.98)			
(30) Priority Data: 08/910,629 13 August 1997 (13.08.97) US		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).	
(63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application US 08/910,629 (CIP) Filed on 13 August 1997 (13.08.97)			
(71) Applicant (for all designated States except US): ISIS PHARMACEUTICALS, INC. [US/US]; Carlsbad Research Center, 2292 Faraday Avenue, Carlsbad, CA 92008 (US).		Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(72) Inventors; and (75) Inventors/Applicants (for US only): McKAY, Robert [US/US]; 2277 Caminito Pescado #73, San Diego, CA 92107 (US). DEAN, Nicholas [GB/US]; 1614 Landquist Drive, Encinitas, CA 92024 (US). MONIA, Brett, P. [US/US]; 7605 Nueva Castilla Way, La Costa, CA 92009 (US). NERO, Pamela, Scott [US/US]; 1010 S. Nevada Street, Oceanside, CA 92054 (US). GAARDE, William, A. [US/US]; 3105 Quebrada Circle, Carlsbad, CA 92009 (US).			

(54) Title: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS FOR THE MODULATION OF JNK PROTEINS

(57) Abstract

Compositions and methods for the treatment and diagnosis of diseases or disorders amenable to treatment through modulation of expression of a gene encoding a Jun N-terminal kinase (JNK protein) are provided. Oligonucleotide are herein provided which are specifically hybridizable with nucleic acids encoding JNK1, JNK2 and JNK3, as well as other JNK proteins and specific isoforms thereof. Methods of treating animals suffering from diseases or disorders amenable to therapeutic intervention by modulating the expression of one or more JNK proteins with such oligonucleotide are also provided. Methods for the treatment and diagnosis of diseases or disorders associated with aberrant expression of one or more JNK proteins are also provided. The invention is thus directed to compositions for modulating, diagnostic methods for detecting, and therapeutic methods for inhibiting, the hyperproliferation of cells and formation, development and maintenance of tumors.

190

**FOR THE PURPOSES OF INFORMATION ONLY**

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece			TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	NZ	New Zealand		
CM	Cameroon			PL	Poland		
CN	China	KR	Republik of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

- 1 -

**ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS  
FOR THE MODULATION OF JNK PROTEINS**

**INTRODUCTION**

This application is a continuation-in-part of U.S.  
5 Application Serial No. 08/910,629 filed August 13, 1997.

**FIELD OF THE INVENTION**

The present invention provides compositions and methods for detecting and modulating levels of Jun N-terminal kinases (JNK proteins), enzymes which are encoded 10 by JNK genes. In particular, the invention relates to antisense oligonucleotides specifically hybridizable with nucleic acids encoding JNK proteins. It has been found that antisense oligonucleotides can modulate the expression of these and other JNK proteins, kinases which were 15 initially discovered due to their ability to catalyze the phosphorylation of the c-Jun subunit of transcription factor AP-1 and thereby increase AP-1 activity. Other transcription factors, such as ATF-2, are similarly activated by JNK proteins, and a variety of other cellular 20 effectors may serve as substrates for JNK proteins (Gupta et al., *Science*, 1995, 267, 389). In any event, transcription factor AP-1 has been implicated in abnormal cell proliferation, oncogenic transformation, and tumor formation, development and maintenance (Vogt, Chapter 15 25 *In: The FOS and JUN Families of Transcription Factors*, Angel and Herrlich, Eds., CRC Press, Boca Raton, FL, 1994).

- 2 -

Accordingly, it is believed that (1) JNK proteins are aberrantly expressed in some neoplasms and tumors with resultant increased AP-1 activity, and (2) even in abnormally proliferating cells in which a JNK gene is not 5 aberrantly expressed, inhibition of JNK expression will result in decreased AP-1 activity and thus, inhibition of abnormal cell proliferation and tumor formation, development and maintenance. The invention is thus directed to diagnostic methods for detecting, and 10 therapeutic methods for inhibiting, the hyperproliferation of cells and the formation, development and maintenance of tumors. Furthermore, this invention is directed to treatment of conditions associated with abnormal expression of JNK genes. This invention also relates to therapies, 15 diagnostics, and research reagents for disease states or disorders which respond to modulation of the expression of JNK proteins. Inhibition of the hyperproliferation of cells, and corresponding prophylactic, palliative and therapeutic effects result from treatment with the 20 oligonucleotides of the invention.

#### **BACKGROUND OF THE INVENTION**

Transcription factors play a central role in the expression of specific genes upon stimulation by extracellular signals, thereby regulating a complex array 25 of biological processes. Members of the family of transcription factors termed AP-1 (activating protein-1) alter gene expression in response to growth factors, cytokines, tumor promoters, carcinogens and increased expression of certain oncogenes (Rahmsdorf, Chapter 13, and 30 Rapp et al., Chapter 16 In: *The FOS and JUN Families of Transcription Factors*, Angel and Herrlich, Eds., CRC Press, Boca Raton, FL, 1994). Growth factors and cytokines exert

- 3 -

their function by binding to specific cell surface receptors. Receptor occupancy triggers a signal transduction cascade to the nucleus. In this cascade, transcription factors such as AP-1 execute long term responses to the extracellular factors by modulating gene expression. Such changes in cellular gene expression lead to DNA synthesis, and eventually the formation of differentiated derivatives (Angel and Karin, *Biochim. Biophys. Acta*, 1991, 1072, 129).

In general terms, AP-1 denotes one member of a family of related heterodimeric transcription factor complexes found in eukaryotic cells or viruses (*The FOS and JUN Families of Transcription Factors*, Angel and Herrlich, Eds., CRC Press, Boca Raton, FL, 1994; Bohmann et al., *Science*, 1987, 238, 1386; Angel et al., *Nature*, 1988, 332, 166). Two relatively well-characterized AP-1 subunits are c-Fos and c-Jun; these two proteins are products of the *c-fos* and *c-jun* proto-oncogenes, respectively. Repression of the activity of either *c-fos* or *c-jun*, or of both proto-oncogenes, and the resultant inhibition of the formation of c-Fos and c-Jun proteins, is desirable for the inhibition of cell proliferation, tumor formation and tumor growth.

The phosphorylation of proteins plays a key role in the transduction of extracellular signals into the cell.

Mitogen-activated protein kinases (MAPKs), enzymes which effect such phosphorylations are targets for the action of growth factors, hormones, and other agents involved in cellular metabolism, proliferation and differentiation (Cobb et al., *J. Biol. Chem.*, 1995, 270, 14843). MAPKs (also referred to as extracellular signal-regulated protein kinases, or ERKs) are themselves activated by phosphorylation catalyzed by, e.g., receptor tyrosine kinases, G protein-coupled receptors, protein kinase C

- 4 -

(PKC), and the apparently MAPK-dedicated kinases MEK1 and MEK2. In general, MAP kinases are involved in a variety of signal transduction pathways (sometimes overlapping and sometimes parallel) that function to convey extracellular stimuli to protooncogene products to modulate cellular proliferation and/or differentiation (Seger et al., *FASEB J.*, 1995, 9, 726; Cano et al., *Trends Biochem. Sci.*, 1995, 20, 117). In a typical MAP kinase pathway, it is thought that a first MAP kinase, called a MEKK, phosphorylates and thereby activates a second MAP kinase, called a MEK, which, in turn, phosphorylates and activates a MAPK/ERK or JNK/SAPK enzyme ("SAPK" is an abbreviation for stress-activated protein kinase). Finally, the activated MAPK/ERK or JNK/SAPK enzyme itself phosphorylates and activates a transcription factor (such as, e.g., AP-1) or other substrates (Cano et al., *Trends Biochem. Sci.*, 1995, 20, 117). This canonical cascade can be simply represented as follows:

MEKK -----> MEK -----> MAPK/ERK -----> transcription factor  
20 or JNK/SAPK or other substrate(s)

One of the signal transduction pathways involves the MAP kinases Jun N-terminal kinase 1 (JNK1) and Jun N-terminal kinase 2 (JNK2) which are responsible for the phosphorylation of specific sites (Serine 63 and Serine 73) on the amino terminal portion of c-Jun. Phosphorylation of these sites potentiates the ability of AP-1 to activate transcription (Binetruy et al., *Nature*, 1991, 351, 122; Smeal et al., *Nature*, 1991, 354, 494). Besides JNK1 and JNK2, other JNK family members have been described, 25 including JNK3 (Gupta et al., *EMBO J.*, 1996, 15, 2760), 30 initially named p49<sup>3F12</sup> kinase (Mohit et al., *Neuron*, 1994,

- 5 -

14, 67). The term "JNK protein" as used herein shall mean a member of the JNK family of kinases, including but not limited to JNK1, JNK2 and JNK3, their isoforms (Gupta et al., *EMBO J.*, 1996, 15, 2760) and other members of the JNK 5 family of proteins whether they function as Jun N-terminal kinases *per se* (that is, phosphorylate Jun at a specific amino terminally located position), or not.

At least one human leukemia oncogene has been shown to enhance Jun N-terminal kinase function (Raitano et al., 10 *Proc. Natl. Acad. Sci. (USA)*, 1995, 92, 11746). Modulation of the expression of one or more JNK proteins is desirable in order to interfere with hyperproliferation of cells and with the transcription of genes stimulated by AP-1 and other JNK protein phosphorylation substrates. Modulation 15 of the expression of one or more other JNK proteins is also desirable in order to interfere with hyperproliferation of cells resulting from abnormalities in specific signal transduction pathways. To date, there are no known therapeutic agents which effectively inhibit gene 20 expression of one or more JNK proteins. Consequently, there remains a long-felt need for improved compositions and methods for modulating the expression of specific JNK proteins.

Moreover, cellular hyperproliferation in an animal 25 can have several outcomes. Internal processes may eliminate hyperproliferative cells before a tumor can form. Tumors are abnormal growths resulting from the hyperproliferation of cells. Cells that proliferate to excess but stay put form benign tumors, which can typically 30 be removed by local surgery. In contrast, malignant tumors or cancers comprise cells that are capable of undergoing metastasis, i.e., a process by which hyperproliferative cells spread to, and secure themselves within, other parts

- 6 -

of the body via the circulatory or lymphatic system (see, generally, Chapter 16 *In: Molecular Biology of the Cell*, Alberts et al., eds., Garland Publishing, Inc., New York, 1983). Using antisense oligonucleotides, it has  
5 surprisingly been discovered that several genes encoding enzymes required for metastasis are positively regulated by AP-1, which may itself be modulated by antisense oligonucleotides targeted to one or more JNK proteins. Consequently, the invention satisfies the long-felt need  
10 for improved compositions and methods for modulating the metastasis of malignant tumors.

#### SUMMARY OF THE INVENTION

In accordance with the present invention, oligonucleotides are provided which specifically hybridize  
15 with a nucleic acid encoding a JNK protein. Certain oligonucleotides of the invention are designed to bind either directly to mRNA transcribed from, or to a selected DNA portion of, a JNK gene that encodes a JNK protein, thereby modulating the expression thereof and/or the  
20 phosphorylation of one or more substrates for the JNK protein. Pharmaceutical compositions comprising the oligonucleotides of the invention, and various methods of using the oligonucleotides of the invention, including methods of modulating one or more metastatic events, are  
25 also herein provided.

#### DETAILED DESCRIPTION OF THE INVENTION

Oligonucleotides may comprise nucleotide sequences sufficient in identity and number to effect specific hybridization with a particular nucleic acid. Such  
30 oligonucleotides are commonly described as "antisense." Antisense oligonucleotides are commonly used as research

- 7 -

reagents, diagnostic aids, and therapeutic agents. It has been discovered that genes (JNK) encoding Jun N-terminal kinase (JNK proteins) are particularly amenable to this approach. In the context of the invention, the terms "Jun 5 N-terminal kinase" and "JNK protein" refer to proteins actually known to phosphorylate the amino terminal (N-terminal) portion of the Jun subunit of AP-1, as well as those that have been tentatively identified as JNK proteins based on amino acid sequence but which may in fact 10 additionally or alternatively bind and/or phosphorylate either other transcription factors (e.g., ATF2) or kinase substrates that are not known to be involved in transcription (Derijard et al., *Cell*, 1994, 76, 1025; Kallunki et al., *Genes & Development*, 1994, 8, 2996; Gupta 15 et al., *EMBO J.*, 1996, 15, 2760). More specifically, the present invention is directed to antisense oligonucleotides that modulate the JNK1, JNK2 and JNK3 proteins. As a consequence of the association between cellular proliferation and activation (via phosphorylation) of AP-1, 20 other transcription factors and/or other proteins by JNK proteins, inhibition of the expression of one or more JNK proteins leads to inhibition of the activation of AP-1 and/or other factors involved in cellular proliferation, cell cycle progression or metastatic events, and, 25 accordingly, results in modulation of these activities. Such modulation is desirable for treating, alleviating or preventing various hyperproliferative disorders or diseases, such as various cancers. Such inhibition is further desirable for preventing or modulating the 30 development of such diseases or disorders in an animal suspected of being, or known to be, prone to such diseases or disorders. If desired, modulation of the expression of one JNK protein can be combined with modulation of one or

- 8 -

more additional JNK proteins in order to achieve a requisite level of interference with AP-1-mediated transcription.

Methods of modulating the expression of JNK proteins comprising contacting animals with oligonucleotides specifically hybridizable with a nucleic acid encoding a JNK protein are herein provided. These methods are believed to be useful both therapeutically and diagnostically as a consequence of the association between kinase-mediated activation of AP-1 and cellular proliferation. These methods are also useful as tools, for example, in the detection and determination of the role of kinase-mediated activation of AP-1 in various cell functions and physiological processes and conditions, and for the diagnosis of conditions associated with such expression and activation.

The present invention also comprises methods of inhibiting JNK-mediated activation using the oligonucleotides of the invention. Methods of treating conditions in which abnormal or excessive JNK-mediated cellular proliferation occurs are also provided. These methods employ the oligonucleotides of the invention and are believed to be useful both therapeutically and as clinical research and diagnostic tools. The oligonucleotides of the present invention may also be used for research purposes. Thus, the specific hybridization exhibited by the oligonucleotides of the present invention may be used for assays, purifications, cellular product preparations and in other methodologies which may be appreciated by persons of ordinary skill in the art.

The present invention employs oligonucleotides for use in antisense modulation of the function of DNA or messenger RNA (mRNA) encoding a protein the modulation of which is desired, and ultimately to regulate the amount of

- 9 -

such a protein. Hybridization of an antisense oligonucleotide with its mRNA target interferes with the normal role of mRNA and causes a modulation of its function in cells. The functions of mRNA to be interfered with 5 include all vital functions such as translocation of the RNA to the site for protein translation, actual translation of protein from the RNA, splicing of the RNA to yield one or more mRNA species, and possibly even independent catalytic activity which may be engaged in by the RNA. The 10 overall effect of such interference with mRNA function is modulation of the expression of a protein, wherein "modulation" means either an increase (stimulation) or a decrease (inhibition) in the expression of the protein. In the context of the present invention, inhibition is the 15 preferred form of modulation of gene expression.

It is preferred to target specific genes for antisense attack. "Targeting" an oligonucleotide to the associated nucleic acid, in the context of this invention, is a multistep process. The process usually begins with 20 the identification of a nucleic acid sequence whose function is to be modulated. This may be, for example, a cellular gene (or mRNA transcribed from the gene) whose expression is associated with a particular disorder or disease state, or a foreign nucleic acid from an infectious 25 agent. In the present invention, the target is a cellular gene associated with hyperproliferative disorders. The targeting process also includes determination of a site or sites within this gene for the oligonucleotide interaction to occur such that the desired effect, either detection or 30 modulation of expression of the protein, will result. Once the target site or sites have been identified, oligonucleotides are chosen which are sufficiently complementary to the target, i.e., hybridize sufficiently

- 10 -

well and with sufficient specificity to give the desired effect. Generally, there are five regions of a gene that may be targeted for antisense modulation: the 5' untranslated region (hereinafter, the "5'-UTR"), the 5 translation initiation codon region (hereinafter, the "tIR"), the open reading frame (hereinafter, the "ORF"), the translation termination codon region (hereinafter, the "tTR") and the 3' untranslated region (hereinafter, the "3'-UTR"). As is known in the art, these regions are 10 arranged in a typical messenger RNA molecule in the following order (left to right, 5' to 3'): 5'-UTR, tIR, ORF, tTR, 3'-UTR. As is known in the art, although some eukaryotic transcripts are directly translated, many ORFs contain one or more sequences, known as "introns," which 15 are excised from a transcript before it is translated; the expressed (unexcised) portions of the ORF are referred to as "exons" (Alberts et al., *Molecular Biology of the Cell*, 1983, Garland Publishing Inc., New York, pp. 411-415). Furthermore, because many eukaryotic ORFs are a thousand 20 nucleotides or more in length, it is often convenient to subdivide the ORF into, e.g., the 5' ORF region, the central ORF region, and the 3' ORF region. In some instances, an ORF contains one or more sites that may be targeted due to some functional significance *in vivo*. 25 Examples of the latter types of sites include intragenic stem-loop structures (see, e.g., U.S. Patent No. 5,512,438) and, in unprocessed mRNA molecules, intron/exon splice sites.

Within the context of the present invention, one 30 preferred intragenic site is the region encompassing the translation initiation codon of the open reading frame (ORF) of the gene. Because, as is known in the art, the translation initiation codon is typically 5'-AUG (in

- 11 -

transcribed mRNA molecules; 5'-ATG in the corresponding DNA molecule), the translation initiation codon is also referred to as the "AUG codon," the "start codon" or the "AUG start codon." A minority of genes have a translation 5 initiation codon having the RNA sequence 5'-GUG, 5'-UUG or 5'-CUG, and 5'-AUA, 5'-ACG and 5'-CUG have been shown to function *in vivo*. Furthermore, 5'-UUU functions as a translation initiation codon *in vitro* (Brigstock et al., *Growth Factors*, 1990, 4, 45; Gelbert et al., *Somat. Cell.* 10 *Mol. Genet.*, 1990, 16, 173; Gold and Stormo, in: *Escherichia coli and Salmonella typhimurium: Cellular and Molecular Biology*, Vol. 2, 1987, Neidhardt et al., eds., American Society for Microbiology, Washington, D.C., p. 1303). Thus, the terms "translation initiation codon" and 15 "start codon" can encompass many codon sequences, even though the initiator amino acid in each instance is typically methionine (in eukaryotes) or formylmethionine (prokaryotes). It is also known in the art that eukaryotic and prokaryotic genes may have two or more alternative 20 start codons, any one of which may be preferentially utilized for translation initiation in a particular cell type or tissue, or under a particular set of conditions, in order to generate related polypeptides having different amino terminal sequences (Markussen et al., *Development*, 25 1995, 121, 3723; Gao et al., *Cancer Res.*, 1995, 55, 743; McDermott et al., *Gene*, 1992, 117, 193; Perri et al., *J. Biol. Chem.*, 1991, 266, 12536; French et al., *J. Virol.*, 1989, 63, 3270; Pushpa-Rekha et al., *J. Biol. Chem.*, 1995, 270, 26993; Monaco et al., *J. Biol. Chem.*, 1994, 269, 347; 30 DeVirgilio et al., *Yeast*, 1992, 8, 1043; Kanagasundaram et al., *Biochim. Biophys. Acta*, 1992, 1171, 198; Olsen et al., *Mol. Endocrinol.*, 1991, 5, 1246; Saul et al., *Appl. Environ. Microbiol.*, 1990, 56, 3117; Yaoita et al., *Proc.*

- 12 -

*Natl. Acad. Sci. USA*, 1990, 87, 7090; Rogers et al., *EMBO J.*, 1990, 9, 2273). In the context of the invention, "start codon" and "translation initiation codon" refer to the codon or codons that are used *in vivo* to initiate translation of an mRNA molecule transcribed from a gene encoding a JNK protein, regardless of the sequence(s) of such codons. It is also known in the art that a translation termination codon (or "stop codon") of a gene may have one of three sequences, i.e., 5'-UAA, 5'-UAG and 5'-UGA (the corresponding DNA sequences are 5'-TAA, 5'-TAG and 5'-TGA, respectively). The terms "start codon region" and "translation initiation region" refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation initiation codon. Similarly, the terms "stop codon region" and "translation termination region" refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation termination codon.

The remainder of the Detailed Description relates in more detail the (1) Oligonucleotides of the Invention and their (2) Bioequivalents, (3) Utility, (4) Pharmaceutical Compositions and (5) Means of Administration.

25       **1. Oligonucleotides of the Invention:** The present invention employs oligonucleotides for use in antisense modulation of one or more JNK proteins. In the context of this invention, the term "oligonucleotide" refers to an oligomer or polymer of ribonucleic acid or deoxyribonucleic acid. This term includes oligonucleotides composed of naturally-occurring nucleobases, sugars and covalent intersugar (backbone) linkages as well as oligonucleotides having non-naturally-occurring portions which function

- 13 -

similarly. Such modified or substituted oligonucleotides are often preferred over native forms because of desirable properties such as, for example, enhanced cellular uptake, enhanced binding to target and increased stability in the  
5 presence of nucleases.

An oligonucleotide is a polymer of a repeating unit generically known as a nucleotide. The oligonucleotides in accordance with this invention preferably comprise from about 8 to about 30 nucleotides. An unmodified (naturally  
10 occurring) nucleotide has three components: (1) a nitrogen-containing heterocyclic base linked by one of its nitrogen atoms to (2) a 5-pentofuranosyl sugar and (3) a phosphate esterified to one of the 5' or 3' carbon atoms of the sugar. When incorporated into an oligonucleotide chain,  
15 the phosphate of a first nucleotide is also esterified to an adjacent sugar of a second, adjacent nucleotide via a 3'-5' phosphate linkage. The "backbone" of an unmodified oligonucleotide consists of (2) and (3), that is, sugars linked together by phosphodiester linkages between the 5'  
20 carbon of the sugar of a first nucleotide and the 3' carbon of a second, adjacent nucleotide. A "nucleoside" is the combination of (1) a nucleobase and (2) a sugar in the absence of (3) a phosphate moiety (Kornberg, A., *DNA Replication*, W.H. Freeman & Co., San Francisco, 1980, pages  
25 4-7). The backbone of an oligonucleotide positions a series of bases in a specific order; the written representation of this series of bases, which is conventionally written in 5' to 3' order, is known as a nucleotide sequence.

30 Oligonucleotides may comprise nucleotide sequences sufficient in identity and number to effect specific hybridization with a particular nucleic acid. Such oligonucleotides which specifically hybridize to a portion

- 14 -

of the sense strand of a gene are commonly described as "antisense." In the context of the invention, "hybridization" means hydrogen bonding, which may be Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding, between complementary nucleotides. For example, adenine and thymine are complementary nucleobases which pair through the formation of hydrogen bonds.

"Complementary," as used herein, refers to the capacity for precise pairing between two nucleotides. For example, if a nucleotide at a certain position of an oligonucleotide is capable of hydrogen bonding with a nucleotide at the same position of a DNA or RNA molecule, then the oligonucleotide and the DNA or RNA are considered to be complementary to each other at that position. The oligonucleotide and the DNA or RNA are complementary to each other when a sufficient number of corresponding positions in each molecule are occupied by nucleotides which can hydrogen bond with each other. Thus, "specifically hybridizable" and "complementary" are terms which are used to indicate a sufficient degree of complementarity or precise pairing such that stable and specific binding occurs between the oligonucleotide and the DNA or RNA target. An oligonucleotide is specifically hybridizable to its target sequence due to the formation of base pairs between specific partner nucleobases in the interior of a nucleic acid duplex. Among the naturally occurring nucleobases, guanine (G) binds to cytosine (C), and adenine (A) binds to thymine (T) or uracil (U). In addition to the equivalency of U (RNA) and T (DNA) as partners for A, other naturally occurring nucleobase equivalents are known, including 5-methylcytosine, 5-hydroxymethylcytosine (HMC), glycosyl HMC and gentiobiosyl HMC (C equivalents), and 5-hydroxymethyluracil (U equivalent). Furthermore, synthetic nucleobases which retain partner specificity are known in

- 15 -

the art and include, for example, 7-deaza-Guanine, which retains partner specificity for C. Thus, an oligonucleotide's capacity to specifically hybridize with its target sequence will not be altered by any chemical  
5 modification to a nucleobase in the nucleotide sequence of the oligonucleotide which does not significantly effect its specificity for the partner nucleobase in the target oligonucleotide. It is understood in the art that an oligonucleotide need not be 100% complementary to its  
10 target DNA sequence to be specifically hybridizable. An oligonucleotide is specifically hybridizable when there is a sufficient degree of complementarity to avoid non-specific binding of the oligonucleotide to non-target sequences under conditions in which specific binding is  
15 desired, i.e., under physiological conditions in the case of *in vivo* assays or therapeutic treatment, or in the case of *in vitro* assays, under conditions in which the assays are performed.

Antisense oligonucleotides are commonly used as  
20 research reagents, diagnostic aids, and therapeutic agents. For example, antisense oligonucleotides, which are able to inhibit gene expression with exquisite specificity, are often used by those of ordinary skill to elucidate the function of particular genes, for example to distinguish  
25 between the functions of various members of a biological pathway. This specific inhibitory effect has, therefore, been harnessed by those skilled in the art for research uses. The specificity and sensitivity of oligonucleotides is also harnessed by those of skill in the art for  
30 therapeutic uses.

**A. Modified Linkages:** Specific examples of some preferred modified oligonucleotides envisioned for this invention include those containing phosphorothioates,

- 16 -

phosphotriesters, methyl phosphonates, short chain alkyl or cycloalkyl intersugar linkages or short chain heteroatomic or heterocyclic intersugar linkages. Most preferred are oligonucleotides with phosphorothioates and those with CH<sub>2</sub>-

5 NH-O-CH<sub>2</sub>, CH<sub>2</sub>-N(CH<sub>3</sub>)-O-CH<sub>2</sub> [known as a methylene(methylimino) or MMI backbone], CH<sub>2</sub>-O-N(CH<sub>3</sub>)-CH<sub>2</sub>, CH<sub>2</sub>-N(CH<sub>3</sub>)-N(CH<sub>3</sub>)-CH<sub>2</sub> and O-N(CH<sub>3</sub>)-CH<sub>2</sub>-CH<sub>2</sub> backbones, wherein the native phosphodiester backbone is represented as O-P-O-CH<sub>2</sub>). Also preferred are oligonucleotides having morpholino backbone structures

10 (Summerton and Weller, U.S. Patent No. 5,034,506). Further preferred are oligonucleotides with NR-C(\*)-CH<sub>2</sub>-CH<sub>2</sub>, CH<sub>2</sub>-NR-C(\*)-CH<sub>2</sub>, CH<sub>2</sub>-CH<sub>2</sub>-NR-C(\*), C(\*)-NR-CH<sub>2</sub>-CH<sub>2</sub> and CH<sub>2</sub>-C(\*)-NR-CH<sub>2</sub> backbones, wherein "\*" represents O or S (known as amide backbones; DeMesmaeker et al., WO 92/20823, published

15 November 26, 1992). In other preferred embodiments, such as the peptide nucleic acid (PNA) backbone, the phosphodiester backbone of the oligonucleotide is replaced with a polyamide backbone, the nucleobases being bound directly or indirectly to the aza nitrogen atoms of the

20 polyamide backbone (Nielsen et al., Science, 1991, 254:1497; U.S. Patent No. 5,539,082).

**B. Modified Nucleobases:** The oligonucleotides of the invention may additionally or alternatively include nucleobase modifications or substitutions. As used herein, 25 "unmodified" or "natural" nucleobases include adenine (A), guanine (G), thymine (T), cytosine (C) and uracil (U). Modified nucleobases include nucleobases found only infrequently or transiently in natural nucleic acids, e.g., hypoxanthine, 6-methyladenine, 5-methylcytosine, 5-hydroxymethylcytosine (HMC), glycosyl HMC and gentiobiosyl HMC, as well synthetic nucleobases, e.g., 2-aminoadenine, 2-thiouracil, 2-thiothymine, 5-bromouracil, 5-hydroxymethyluracil, 8-azaguanine, 7-deazaguanine, N<sup>6</sup>(6-

- 17 -

aminohexyl)adenine and 2,6-diaminopurine (Kornberg, A., *DNA Replication*, W.H. Freeman & Co., San Francisco, 1980, pages 75-77; Gebeyehu, G., et al., *Nucleic Acids Res.*, 1987, 15, 4513).

5           **C. Sugar Modifications:** The oligonucleotides of the invention may additionally or alternatively comprise substitutions of the sugar portion of the individual nucleotides. For example, oligonucleotides may also have sugar mimetics such as cyclobutylys in place of the  
10 pentofuranosyl group. Other preferred modified oligonucleotides may contain one or more substituted sugar moieties comprising one of the following at the 2' position: OH, SH, SCH<sub>3</sub>, F, OCN, OCH<sub>3</sub>OCH<sub>3</sub>, OCH<sub>3</sub>O(CH<sub>2</sub>)<sub>n</sub>CH<sub>3</sub>, O(CH<sub>2</sub>)<sub>n</sub>NH<sub>2</sub> or O(CH<sub>2</sub>)<sub>n</sub>CH<sub>3</sub>, where n is from 1 to about 10; C<sub>1</sub> to  
15 C<sub>10</sub> lower alkyl, alkoxyalkoxy, substituted lower alkyl, alkaryl or aralkyl; Cl; Br; CN; CF<sub>3</sub>; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; SOCH<sub>3</sub>; SO<sub>2</sub>CH<sub>3</sub>; ONO<sub>2</sub>; NO<sub>2</sub>; N<sub>3</sub>; NH<sub>2</sub>; heterocycloalkyl; heterocycloalkaryl; aminoalkylamino; polyalkylamino; substituted silyl; an RNA cleaving group; a  
20 reporter group; an intercalator; a group for improving the pharmacokinetic properties of an oligonucleotide; or a group for improving the pharmacodynamic properties of an oligonucleotide and other substituents having similar properties. A preferred modification includes 2'-methoxyethoxy [2'-O-CH<sub>2</sub>CH<sub>2</sub>OCH<sub>3</sub>, also known as 2'-O-(2-methoxyethyl)] (Martin et al., *Helv. Chim. Acta*, 1995, 78:486). Other preferred modifications include 2'-methoxy-(2'-O-CH<sub>3</sub>), 2'-propoxy- (2'-OCH<sub>2</sub>CH<sub>2</sub>CH<sub>3</sub>) and 2'-fluoro- (2'-F).

30           **D. Other Modifications:** Similar modifications may also be made at other positions on the oligonucleotide, particularly the 3' position of the sugar on the 3' terminal nucleotide and the 5' position of 5' terminal

- 18 -

nucleotide. The 5' and 3' termini of an oligonucleotide may also be modified to serve as points of chemical conjugation of, e.g., lipophilic moieties (see immediately subsequent paragraph), intercalating agents (Kuyavin et al., WO 96/32496, published October 17, 1996; Nguyen et al., U.S. Patent No. 4,835,263, issued May 30, 1989) or hydroxyalkyl groups (Helene et al., WO 96/34008, published October 31, 1996).

Other positions within an oligonucleotide of the invention can be used to chemically link thereto one or more effector groups to form an oligonucleotide conjugate. An "effector group" is a chemical moiety that is capable of carrying out a particular chemical or biological function. Examples of such effector groups include, but are not limited to, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide and other substituents having similar properties. A variety of chemical linkers may be used to conjugate an effector group to an oligonucleotide of the invention. As an example, U.S. Patent No. 5,578,718 to Cook et al. discloses methods of attaching an alkylthio linker, which may be further derivatized to include additional groups, to ribofuranosyl positions, nucleosidic base positions, or on internucleoside linkages. Additional methods of conjugating oligonucleotides to various effector groups are known in the art; see, e.g., *Protocols for Oligonucleotide Conjugates (Methods in Molecular Biology, Volume 26)* 25 30 Agrawal, S., ed., Humana Press, Totowa, NJ, 1994.

Another preferred additional or alternative modification of the oligonucleotides of the invention involves chemically linking to the oligonucleotide one or

more lipophilic moieties which enhance the cellular uptake of the oligonucleotide. Such lipophilic moieties may be linked to an oligonucleotide at several different positions on the oligonucleotide. Some preferred positions include  
5 the 3' position of the sugar of the 3' terminal nucleotide, the 5' position of the sugar of the 5' terminal nucleotide, and the 2' position of the sugar of any nucleotide. The N<sup>6</sup> position of a purine nucleobase may also be utilized to link a lipophilic moiety to an oligonucleotide of the  
10 invention (Gebeyehu, G., et al., *Nucleic Acids Res.*, 1987, 15:4513). Such lipophilic moieties include but are not limited to a cholesteryl moiety (Letsinger et al., *Proc. Natl. Acad. Sci. U.S.A.*, 1989, 86:6553), cholic acid (Manoharan et al., *Bioorg. Med. Chem. Lett.*, 1994, 4:1053),  
15 a thioether, e.g., hexyl-S-tritylthiol (Manoharan et al., *Ann. N.Y. Acad. Sci.*, 1992, 660:306; Manoharan et al., *Bioorg. Med. Chem. Lett.*, 1993, 3:2765), a thiocholesterol (Oberhauser et al., *Nucl. Acids Res.*, 1992, 20:533), an aliphatic chain, e.g., dodecandiol or undecyl residues  
20 (Saison-Behmoaras et al., *EMBO J.*, 1991, 10:111; Kabanov et al., *FEBS Lett.*, 1990, 259:327; Svinarchuk et al., *Biochimie*, 1993, 75:49), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan et al.,  
25 *Tetrahedron Lett.*, 1995, 36:3651; Shea et al., *Nucl. Acids Res.*, 1990, 18:3777), a polyamine or a polyethylene glycol chain (Manoharan et al., *Nucleosides & Nucleotides*, 1995, 14:969), or adamantan acetic acid (Manoharan et al., *Tetrahedron Lett.*, 1995, 36:3651), a palmityl moiety  
30 (Mishra et al., *Biochim. Biophys. Acta*, 1995, 1264:229), or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety (Crooke et al., *J. Pharmacol. Exp. Ther.*, 1996, 277:923). Oligonucleotides comprising lipophilic moieties,

- 20 -

and methods for preparing such oligonucleotides, are disclosed in U.S. Patents Nos. 5,138,045, 5,218,105 and 5,459,255.

The present invention also includes oligonucleotides 5 that are substantially chirally pure with regard to particular positions within the oligonucleotides. Examples of substantially chirally pure oligonucleotides include, but are not limited to, those having phosphorothioate linkages that are at least 75% Sp or Rp (Cook et al., U.S. 10 Patent No. 5,587,361) and those having substantially chirally pure (Sp or Rp) alkylphosphonate, phosphoamidate or phosphotriester linkages (Cook, U.S. Patents Nos. 5,212,295 and 5,521,302).

**E. Chimeric Oligonucleotides:** The present 15 invention also includes oligonucleotides which are chimeric oligonucleotides. "Chimeric" oligonucleotides or "chimeras," in the context of this invention, are oligonucleotides which contain two or more chemically distinct regions, each made up of at least one nucleotide. 20 These oligonucleotides typically contain at least one region wherein the oligonucleotide is modified so as to confer upon the oligonucleotide increased resistance to nuclease degradation, increased cellular uptake, and/or increased binding affinity for the target nucleic acid. An 25 additional region of the oligonucleotide may serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNase H is a cellular endonuclease which cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in 30 cleavage of the RNA target, thereby greatly enhancing the efficiency of antisense inhibition of gene expression. Cleavage of the RNA target can be routinely detected by gel electrophoresis and, if necessary, associated nucleic acid

hybridization techniques known in the art. By way of example, such "chimeras" may be "gapmers," i.e., oligonucleotides in which a central portion (the "gap") of the oligonucleotide serves as a substrate for, e.g., RNase H, and the 5' and 3' portions (the "wings") are modified in such a fashion so as to have greater affinity for the target RNA molecule but are unable to support nuclease activity (e.g., 2'-fluoro- or 2'-methoxyethoxy-substituted). Other chimeras include "wingmers," that is, oligonucleotides in which the 5' portion of the oligonucleotide serves as a substrate for, e.g., RNase H, whereas the 3' portion is modified in such a fashion so as to have greater affinity for the target RNA molecule but is unable to support nuclease activity (e.g., 2'-fluoro- or 2'-methoxyethoxy- substituted), or vice-versa.

**F. Synthesis:** The oligonucleotides used in accordance with this invention may be conveniently and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is sold by several vendors including, for example, Applied Biosystems (Foster City, CA). Any other means for such synthesis known in the art may additionally or alternatively be employed. It is also known to use similar techniques to prepare other oligonucleotides such as the phosphorothioates and alkylated derivatives.

**1. Teachings** regarding the synthesis of particular modified oligonucleotides may be found in the following U.S. patents or pending patent applications, each of which is commonly assigned with this application: U.S. Patents Nos. 5,138,045 and 5,218,105, drawn to polyamine conjugated oligonucleotides; U.S. Patent No. 5,212,295, drawn to monomers for the preparation of oligonucleotides having chiral phosphorus linkages; U.S. Patents Nos.

- 22 -

5,378,825 and 5,541,307, drawn to oligonucleotides having modified backbones; U.S. Patent No. 5,386,023, drawn to backbone modified oligonucleotides and the preparation thereof through reductive coupling; U.S. Patent No.

5 5,457,191, drawn to modified nucleobases based on the 3-deazapurine ring system and methods of synthesis thereof; U.S. Patent No. 5,459,255, drawn to modified nucleobases based on N-2 substituted purines; U.S. Patent No.

5,521,302, drawn to processes for preparing

10 oligonucleotides having chiral phosphorus linkages; U.S. Patent No. 5,539,082, drawn to peptide nucleic acids; U.S. Patent No. 5,554,746, drawn to oligonucleotides having β-lactam backbones; U.S. Patent No. 5,571,902, drawn to methods and materials for the synthesis of

15 oligonucleotides; U.S. Patent No. 5,578,718, drawn to nucleosides having alkylthio groups, wherein such groups may be used as linkers to other moieties attached at any of a variety of positions of the nucleoside; U.S. Patents Nos. 5,587,361 and 5,599,797, drawn to oligonucleotides having

20 phosphorothioate linkages of high chiral purity; U.S. Patent No. 5,506,351, drawn to processes for the preparation of 2'-O-alkyl guanosine and related compounds, including 2,6-diaminopurine compounds; U.S. Patent No.

5,587,469, drawn to oligonucleotides having N-2 substituted

25 purines; U.S. Patent No. 5,587,470, drawn to oligonucleotides having 3-deazapurines; U.S. Patents Nos. 5,223,168, issued June 29, 1993, and 5,608,046, both drawn to conjugated 4'-desmethyl nucleoside analogs; U.S. Patent Nos. 5,602,240, and 5,610,289, drawn to backbone modified

30 oligonucleotide analogs; and U.S. patent application Serial No. 08/383,666, filed February 3, 1995, and U.S. Patent No. 5,459,255, drawn to, *inter alia*, methods of synthesizing 2'-fluoro-oligonucleotides.

- 23 -

2. 5-methyl-cytosine: In 2'-methoxyethoxy-modified oligonucleotides, 5-methyl-2'-methoxyethoxy-cytosine residues are used and are prepared as follows.

(a) 2,2'-Anhydro[1-( $\beta$ -D-

5 arabinofuranosyl)-5-methyluridine]: 5-Methyluridine (ribosylthymine, commercially available through Yamasaki, Choshi, Japan) (72.0 g, 0.279 M), diphenylcarbonate (90.0 g, 0.420 M) and sodium bicarbonate (2.0 g, 0.024 M) were added to DMF (300 mL). The mixture was heated to reflux, 10 with stirring, allowing the evolved carbon dioxide gas to be released in a controlled manner. After 1 hour, the slightly darkened solution was concentrated under reduced pressure. The resulting syrup was poured into diethylether (2.5 L), with stirring. The product formed a gum. The 15 ether was decanted and the residue was dissolved in a minimum amount of methanol (ca. 400 mL). The solution was poured into fresh ether (2.5 L) to yield a stiff gum. The ether was decanted and the gum was dried in a vacuum oven (60°C at 1 mm Hg for 24 h) to give a solid which was crushed 20 to a light tan powder (57 g, 85% crude yield). The material was used as is for further reactions.

(b) 2'-O-Methoxyethyl-5-methyluridine:

2,2'-Anhydro-5-methyluridine (195 g, 0.81 M), tris(2-methoxyethyl)borate (231 g, 0.98 M) and 2-methoxyethanol (1.2 L) were added to a 2 L stainless steel pressure vessel 25 and placed in a pre-heated oil bath at 160°C. After heating for 48 hours at 155-160°C, the vessel was opened and the solution evaporated to dryness and triturated with MeOH (200 mL). The residue was suspended in hot acetone (1 L). 30 The insoluble salts were filtered, washed with acetone (150 mL) and the filtrate evaporated. The residue (280 g) was dissolved in CH<sub>3</sub>CN (600 mL) and evaporated. A silica gel column (3 kg) was packed in CH<sub>2</sub>Cl<sub>2</sub>/acetone/MeOH (20:5:3)

- 24 -

containing 0.5% Et<sub>3</sub>NH. The residue was dissolved in CH<sub>2</sub>Cl<sub>2</sub> (250 mL) and adsorbed onto silica (150 g) prior to loading onto the column. The product was eluted with the packing solvent to give 160 g (63%) of product.

5                             (c) 2'-O-Methoxyethyl-5'-O-

dimethoxytrityl-5-methyluridine: 2'-O-Methoxyethyl-5-methyluridine (160 g, 0.506 M) was co-evaporated with pyridine (250 mL) and the dried residue dissolved in pyridine (1.3 L). A first aliquot of dimethoxytrityl 10 chloride (94.3 g, 0.278 M) was added and the mixture stirred at room temperature for one hour. A second aliquot of dimethoxytrityl chloride (94.3 g, 0.278 M) was added and the reaction stirred for an additional one hour. Methanol (170 mL) was then added to stop the reaction. HPLC showed 15 the presence of approximately 70% product. The solvent was evaporated and triturated with CH<sub>3</sub>CN (200 mL). The residue was dissolved in CHCl<sub>3</sub> (1.5 L) and extracted with 2x 500 mL of saturated NaHCO<sub>3</sub> and 2x 500 mL of saturated NaCl. The organic phase was dried over Na<sub>2</sub>SO<sub>4</sub>, filtered and 20 evaporated. 275 g of residue was obtained. The residue was purified on a 3.5 kg silica gel column, packed and eluted with EtOAc/Hexane/Acetone (5:5:1) containing 0.5% Et<sub>3</sub>NH. The pure fractions were evaporated to give 164 g of product. Approximately 20 g additional was obtained from 25 the impure fractions to give a total yield of 183 g (57%).

                           (d) 3'-O-Acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine: 2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine (106 g, 0.167 M), DMF/pyridine (750 mL of a 3:1 mixture prepared from 562 mL 30 of DMF and 188 mL of pyridine) and acetic anhydride (24.38 mL, 0.258 M) were combined and stirred at room temperature for 24 hours. The reaction was monitored by tlc by first quenching the tlc sample with the addition of MeOH. Upon

- 25 -

completion of the reaction, as judged by tlc, MeOH (50 mL) was added and the mixture evaporated at 35°C. The residue was dissolved in CHCl<sub>3</sub> (800 mL) and extracted with 2x 200 mL of saturated sodium bicarbonate and 2x 200 mL of saturated NaCl. The water layers were back extracted with 200 mL of CHCl<sub>3</sub>. The combined organics were dried with sodium sulfate and evaporated to give 122 g of residue (approximately 90% product). The residue was purified on a 3.5 kg silica gel column and eluted using EtOAc/Hexane (4:1). Pure product fractions were evaporated to yield 96 g (84%).

(e) **3'-O-Acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyl-4-triazoleuridine:**

A first solution was prepared by dissolving 3'-O-acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine (96 g, 0.144 M) in CH<sub>3</sub>CN (700 mL) and set aside. Triethylamine (189 mL, 1.44 M) was added to a solution of triazole (90 g, 1.3 M) in CH<sub>3</sub>CN (1 L), cooled to -5°C and stirred for 0.5 h using an overhead stirrer. POCl<sub>3</sub> was added dropwise, over a 30 minute period, to the stirred solution maintained at 0-10°C, and the resulting mixture stirred for an additional 2 hours. The first solution was added dropwise, over a 45 minute period, to the later solution. The resulting reaction mixture was stored overnight in a cold room. Salts were filtered from the reaction mixture and the solution was evaporated. The residue was dissolved in EtOAc (1 L) and the insoluble solids were removed by filtration. The filtrate was washed with 1x 300 mL of NaHCO<sub>3</sub> and 2x 300 mL of saturated NaCl, dried over sodium sulfate and evaporated. The residue was triturated with EtOAc to give the title compound.

(f) **2'-O-Methoxyethyl-5'-O-**

**dimethoxytrityl-5-methylcytidine:** A solution of 3'-O-acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyl-4-

- 26 -

triazoleuridine (103 g, 0.141 M) in dioxane (500 mL) and NH<sub>4</sub>OH (30 mL) was stirred at room temperature for 2 hours. The dioxane solution was evaporated and the residue azeotroped with MeOH (2x 200 mL). The residue was 5 dissolved in MeOH (300 mL) and transferred to a 2 liter stainless steel pressure vessel. Methanol (400 mL) saturated with NH<sub>3</sub> gas was added and the vessel heated to 100°C for 2 hours (thin layer chromatography, tlc, showed complete conversion). The vessel contents were evaporated 10 to dryness and the residue was dissolved in EtOAc (500 mL) and washed once with saturated NaCl (200 mL). The organics were dried over sodium sulfate and the solvent was evaporated to give 85 g (95%) of the title compound.

(g) N<sup>4</sup>-Benzoyl-2'-O-methoxyethyl-5'-O-

15 **dimethoxytrityl-5-methylcytidine:** 2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine (85 g, 0.134 M) was dissolved in DMF (800 mL) and benzoic anhydride (37.2 g, 0.165 M) was added with stirring. After stirring for 3 hours, tlc showed the reaction to be approximately 95% 20 complete. The solvent was evaporated and the residue azeotroped with MeOH (200 mL). The residue was dissolved in CHCl<sub>3</sub> (700 mL) and extracted with saturated NaHCO<sub>3</sub> (2x 300 mL) and saturated NaCl (2x 300 mL), dried over MgSO<sub>4</sub>, and evaporated to give a residue (96 g). The residue was 25 chromatographed on a 1.5 kg silica column using EtOAc/Hexane (1:1) containing 0.5% Et<sub>3</sub>NH as the eluting solvent. The pure product fractions were evaporated to give 90 g (90%) of the title compound.

(h) N<sup>4</sup>-Benzoyl-2'-O-methoxyethyl-5'-O-

30 **dimethoxytrityl-5-methylcytidine-3'-amidite:** N<sup>4</sup>-Benzoyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine (74 g, 0.10 M) was dissolved in CH<sub>2</sub>Cl<sub>2</sub> (1 L). Tetrazole diisopropylamine (7.1 g) and 2-cyanoethoxy-tetra-

- 27 -

(isopropyl)phosphite (40.5 mL, 0.123 M) were added with stirring, under a nitrogen atmosphere. The resulting mixture was stirred for 20 hours at room temperature (tlc showed the reaction to be 95% complete). The reaction 5 mixture was extracted with saturated NaHCO<sub>3</sub> (1x 300 mL) and saturated NaCl (3x 300 mL). The aqueous washes were back-extracted with CH<sub>2</sub>Cl<sub>2</sub> (300 mL), and the extracts were combined, dried over MgSO<sub>4</sub>, and concentrated. The residue obtained was chromatographed on a 1.5 kg silica column 10 using EtOAc\Hexane (3:1) as the eluting solvent. The pure fractions were combined to give 90.6 g (87%) of the title compound.

**2. Bioequivalents:** The compounds of the invention encompass any pharmaceutically acceptable salts, esters, or 15 salts of such esters, or any other compound which, upon administration to an animal including a human, is capable of providing (directly or indirectly) the biologically active metabolite or residue thereof. Accordingly, for example, the disclosure is also drawn to "prodrugs" and 20 "pharmaceutically acceptable salts" of the oligonucleotides of the invention, pharmaceutically acceptable salts of such prodrugs, and other bioequivalents.

**A. Oligonucleotide Prodrugs:** The oligonucleotides of the invention may additionally or 25 alternatively be prepared to be delivered in a "prodrug" form. The term "prodrug" indicates a therapeutic agent that is prepared in an inactive form that is converted to an active form (*i.e.*, drug) within the body or cells thereof by the action of endogenous enzymes or other 30 chemicals and/or conditions. In particular, prodrug versions of the oligonucleotides of the invention are prepared as SATE [(S-acetyl-2-thioethyl) phosphate]

derivatives according to the methods disclosed in WO 93/24510 to Gosselin et al., published December 9, 1993.

- B. Pharmaceutically Acceptable Salts:** The term "pharmaceutically acceptable salts" refers to 5 physiologically and pharmaceutically acceptable salts of the oligonucleotides of the invention: i.e., salts that retain the desired biological activity of the parent compound and do not impart undesired toxicological effects thereto.
- 10       Pharmaceutically acceptable base addition salts are formed with metals or amines, such as alkali and alkaline earth metals or organic amines. Examples of metals used as cations are sodium, potassium, magnesium, calcium, and the like. Examples of suitable amines are
- 15       N,N'-dibenzylethylenediamine, chloroprocaine, choline, diethanolamine, dicyclohexylamine, ethylenediamine, N-methylglucamine, and procaine (see, for example, Berge et al., "Pharmaceutical Salts," *J. of Pharma Sci.*, 1977, 66:1). The base addition salts of said acidic compounds
- 20       are prepared by contacting the free acid form with a sufficient amount of the desired base to produce the salt in the conventional manner. The free acid form may be regenerated by contacting the salt form with an acid and isolating the free acid in the conventional manner. The
- 25       free acid forms differ from their respective salt forms somewhat in certain physical properties such as solubility in polar solvents, but otherwise the salts are equivalent to their respective free acid for purposes of the present invention. As used herein, a "pharmaceutical addition
- 30       salt" includes a pharmaceutically acceptable salt of an acid form of one of the components of the compositions of the invention. These include organic or inorganic acid salts of the amines. Preferred acid salts are the

hydrochlorides, acetates, salicylates, nitrates and phosphates. Other suitable pharmaceutically acceptable salts are well known to those skilled in the art and include basic salts of a variety of inorganic and organic acids, such as, for example, with inorganic acids, such as for example hydrochloric acid, hydrobromic acid, sulfuric acid or phosphoric acid; with organic carboxylic, sulfonic, sulfo or phospho acids or N-substituted sulfamic acids, for example acetic acid, propionic acid, glycolic acid, succinic acid, maleic acid, hydroxymaleic acid, methylmaleic acid, fumaric acid, malic acid, tartaric acid, lactic acid, oxalic acid, gluconic acid, glucaric acid, glucuronic acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, salicylic acid, 4-aminosalicylic acid, 2-phenoxybenzoic acid, 2-acetoxybenzoic acid, embonic acid, nicotinic acid or isonicotinic acid; and with amino acids, such as the 20 alpha-amino acids involved in the synthesis of proteins in nature, for example glutamic acid or aspartic acid, and also with phenylacetic acid, methanesulfonic acid, ethanesulfonic acid, 2-hydroxyethanesulfonic acid, ethane-1,2-disulfonic acid, benzenesulfonic acid, 4-methylbenzenesulfonic acid, naphthalene-2-sulfonic acid, naphthalene-1,5-disulfonic acid, 2- or 3-phosphoglycerate, glucose-6-phosphate, N-cyclohexylsulfamic acid (with the formation of cyclamates), or with other acid organic compounds, such as ascorbic acid. Pharmaceutically acceptable salts of compounds may also be prepared with a pharmaceutically acceptable cation. Suitable pharmaceutically acceptable cations are well known to those skilled in the art and include alkaline, alkaline earth, ammonium and quaternary ammonium cations. Carbonates or hydrogen carbonates are also possible.

- 30 -

For oligonucleotides, preferred examples of pharmaceutically acceptable salts include but are not limited to (a) salts formed with cations such as sodium, potassium, ammonium, magnesium, calcium, polyamines such as 5 spermine and spermidine, etc.; (b) acid addition salts formed with inorganic acids, for example hydrochloric acid, hydrobromic acid, sulfuric acid, phosphoric acid, nitric acid and the like; (c) salts formed with organic acids such as, for example, acetic acid, oxalic acid, tartaric 10 acid, succinic acid, maleic acid, fumaric acid, gluconic acid, citric acid, malic acid, ascorbic acid, benzoic acid, tannic acid, palmitic acid, alginic acid, polyglutamic acid, naphthalenesulfonic acid, methanesulfonic acid, p-toluenesulfonic acid, naphthalenedisulfonic acid, 15 polygalacturonic acid, and the like; and (d) salts formed from elemental anions such as chlorine, bromine, and iodine.

**3. Exemplary Utilities of the Invention:** The oligonucleotides of the present invention specifically 20 hybridize to nucleic acids (e.g., mRNAs) encoding a JNK protein. The oligonucleotides of the present invention can be utilized as therapeutic compounds, as diagnostic tools or research reagents that can be incorporated into kits, and in purifications and cellular product preparations, as 25 well as other methodologies, which are appreciated by persons of ordinary skill in the art.

**A. Assays and Diagnostic Applications:** The oligonucleotides of the present invention can be used to detect the presence of JNK protein-specific nucleic acids 30 in a cell or tissue sample. For example, radiolabeled oligonucleotides can be prepared by <sup>32</sup>P labeling at the 5' end with polynucleotide kinase. (Sambrook et al., *Molecular Cloning. A Laboratory Manual*, Cold Spring Harbor

- 31 -

Laboratory Press, 1989, Volume 2, pg. 10.59.) Radiolabeled oligonucleotides are then contacted with cell or tissue samples suspected of containing JNK protein message RNAs (and thus JNK proteins), and the samples are washed to  
5 remove unbound oligonucleotide. Radioactivity remaining in the sample indicates the presence of bound oligonucleotide, which in turn indicates the presence of nucleic acids complementary to the oligonucleotide, and can be quantitated using a scintillation counter or other routine  
10 means. Expression of nucleic acids encoding these proteins is thus detected.

Radiolabeled oligonucleotides of the present invention can also be used to perform autoradiography of tissues to determine the localization, distribution and  
15 quantitation of JNK proteins for research, diagnostic or therapeutic purposes. In such studies, tissue sections are treated with radiolabeled oligonucleotide and washed as described above, then exposed to photographic emulsion according to routine autoradiography procedures. The  
20 emulsion, when developed, yields an image of silver grains over the regions expressing a JNK protein gene. Quantitation of the silver grains permits detection of the expression of mRNA molecules encoding these proteins and permits targeting of oligonucleotides to these areas.

25 Analogous assays for fluorescent detection of expression of JNK protein nucleic acids can be developed using oligonucleotides of the present invention which are conjugated with fluorescein or other fluorescent tags instead of radiolabeling. Such conjugations are routinely  
30 accomplished during solid phase synthesis using fluorescently-labeled amidites or controlled pore glass (CPG) columns. Fluorescein-labeled amidites and CPG are available from, e.g., Glen Research, Sterling VA. Other

- 32 -

means of labeling oligonucleotides are known in the art (see, e.g., Ruth, Chapter 6 In: *Methods in Molecular Biology, Vol. 26: Protocols for Oligonucleotide Conjugates*, Agrawal, ed., Humana Press Inc., Totowa, NJ, 1994, pages 5 167-185).

Kits for detecting the presence or absence of expression of a JNK protein may also be prepared. Such kits include an oligonucleotide targeted to an appropriate gene, i.e., a gene encoding a JNK protein. Appropriate kit 10 and assay formats, such as, e.g., "sandwich" assays, are known in the art and can easily be adapted for use with the oligonucleotides of the invention. Hybridization of the oligonucleotides of the invention with a nucleic acid encoding a JNK protein can be detected by means known in 15 the art. Such means may include conjugation of an enzyme to the oligonucleotide, radiolabelling of the oligonucleotide or any other suitable detection systems.

**B. Protein Purifications:** The oligonucleotides of the invention are also useful for the purification of 20 specific Jun kinase proteins from cells that normally express a set of JNK proteins which are similar to each other in terms of their polypeptide sequences and biochemical properties. As an example, the purification of a JNK1 protein from cells that expresses JNK1, JNK2 and 25 JNK3 proteins can be enhanced by first treating such cells with oligonucleotides that inhibit the expression of JNK2 and JNK3 and/or with oligonucleotides that increase the expression of JNK1, because such treatments will increase the relative ratio of JNK1 relative to JNK2 and JNK3. As a 30 result, the yield of JNK1 from subsequent purification steps will be improved as the amount of the biochemically similar (and thus likely to contaminate) JNK2 and JNK3

proteins in extracts prepared from cells so treated will be diminished.

**C. Biologically Active Oligonucleotides:** The invention is also drawn to the administration of oligonucleotides having biological activity to cultured cells, isolated tissues and organs and animals. By "having biological activity," it is meant that the oligonucleotide functions to modulate the expression of one or more genes in cultured cells, isolated tissues or organs and/or animals. Such modulation can be achieved by an antisense oligonucleotide by a variety of mechanisms known in the art, including but not limited to transcriptional arrest; effects on RNA processing (capping, polyadenylation and splicing) and transportation; enhancement of cellular degradation of the target nucleic acid; and translational arrest (*Crooke et al., Exp. Opin. Ther. Patents, 1996, 6:855*).

In an animal other than a human, the compositions and methods of the invention can be used to study the function of one or more genes in the animal. For example, antisense oligonucleotides have been systemically administered to rats in order to study the role of the *N*-methyl-D-aspartate receptor in neuronal death, to mice in order to investigate the biological role of protein kinase C- $\alpha$ , and to rats in order to examine the role of the neuropeptide Y1 receptor in anxiety (*Wahlestedt et al., Nature, 1993, 363:260; Dean et al., Proc. Natl. Acad. Sci. U.S.A., 1994, 91:11762; and Wahlestedt et al., Science, 1993, 259:528, respectively*).

In instances where complex families of related proteins are being investigated, "antisense knockouts" (i.e., inhibition of a gene by systemic administration of antisense oligonucleotides) may represent the most accurate means for

examining a specific member of the family (see, generally, Albert et al., *Trends Pharmacol. Sci.*, 1994, 15:250).

The compositions and methods of the invention also have therapeutic uses in an animal, including a human, 5 having (i.e., suffering from), or known to be or suspected of being prone to having, a disease or disorder that is treatable in whole or in part with one or more nucleic acids. The term "therapeutic uses" is intended to encompass prophylactic, palliative and curative uses 10 wherein the oligonucleotides of the invention are contacted with animal cells either *in vivo* or *ex vivo*. When contacted with animal cells *ex vivo*, a therapeutic use includes incorporating such cells into an animal after treatment with one or more oligonucleotides of the 15 invention.

For therapeutic uses, an animal suspected of having a disease or disorder which can be treated or prevented by modulating the expression or activity of a JNK protein is, for example, treated by administering oligonucleotides in 20 accordance with this invention. The oligonucleotides of the invention can be utilized in pharmaceutical compositions by adding an effective amount of an oligonucleotide to a suitable pharmaceutically acceptable carrier such as, e.g., a diluent. Workers in the field 25 have identified antisense, triplex and other oligonucleotide compositions which are capable of modulating expression of genes implicated in viral, fungal and metabolic diseases. Antisense oligonucleotides have been safely administered to humans and several clinical 30 trials are presently underway. It is thus established that oligonucleotides can be useful therapeutic instrumentalities that can be configured to be useful in treatment regimes for treatment of cells, tissues and

- 35 -

animals, especially humans. The following U.S. patents demonstrate palliative, therapeutic and other methods utilizing antisense oligonucleotides. U. S. Patent No. 5,135,917 provides antisense oligonucleotides that inhibit 5 human interleukin-1 receptor expression. U.S. Patent No. 5,098,890 is directed to antisense oligonucleotides complementary to the *c-myb* oncogene and antisense oligonucleotide therapies for certain cancerous conditions. U.S. Patent No. 5,087,617 provides methods for treating 10 cancer patients with antisense oligonucleotides. U.S. Patent No. 5,166,195 provides oligonucleotide inhibitors of Human Immunodeficiency Virus (HIV). U.S. Patent No. 5,004,810 provides oligomers capable of hybridizing to herpes simplex virus Vmw65 mRNA and inhibiting replication. 15 U.S. Patent No. 5,194,428 provides antisense oligonucleotides having antiviral activity against influenza virus. U.S. Patent No. 4,806,463 provides antisense oligonucleotides and methods using them to inhibit HTLV-III replication. U.S. Patent No. 5,286,717 20 provides oligonucleotides having a complementary base sequence to a portion of an oncogene. U.S. Patent No. 5,276,019 and U.S. Patent No. 5,264,423 are directed to phosphorothioate oligonucleotide analogs used to prevent replication of foreign nucleic acids in cells. U.S. Patent 25 No. 4,689,320 is directed to antisense oligonucleotides as antiviral agents specific to cytomegalovirus (CMV). U.S. Patent No. 5,098,890 provides oligonucleotides complementary to at least a portion of the mRNA transcript of the human *c-myb* gene. U.S. Patent No. 5,242,906 30 provides antisense oligonucleotides useful in the treatment of latent Epstein-Barr virus (EBV) infections.

As used herein, the term "disease or disorder" (1) includes any abnormal condition of an organism or part,

- 36 -

especially as a consequence of infection, inherent weakness, environmental stress, that impairs normal physiological functioning; (2) excludes pregnancy *per se* but not autoimmune and other diseases associated with 5 pregnancy; and (3) includes cancers and tumors. The term "known to be or suspected of being prone to having a disease or disorder" indicates that the subject animal has been determined to be, or is suspected of being, at increased risk, relative to the general population of such 10 animals, of developing a particular disease or disorder as herein defined. For example, a subject animal "known to be or suspected of being prone to having a disease or disorder" could have a personal and/or family medical history that includes frequent occurrences of a particular 15 disease or disorder. As another example, a subject animal "known to be or suspected of being prone to having a disease or disorder" could have had such a susceptibility determined by genetic screening according to techniques known in the art (see, e.g., U.S. Congress, Office of 20 Technology Assessment, Chapter 5 *In: Genetic Monitoring and Screening in the Workplace*, OTA-BA-455, U.S. Government Printing Office, Washington, D.C., 1990, pages 75-99). The term "a disease or disorder that is treatable in whole or in part with one or more nucleic acids" refers to a disease 25 or disorder, as herein defined, (1) the management, modulation or treatment thereof, and/or (2) therapeutic, curative, palliative and/or prophylactic relief therefrom, can be provided via the administration of an antisense oligonucleotide.

30       **4. Pharmaceutical Compositions:** The formulation of pharmaceutical compositions comprising the oligonucleotides of the invention, and their subsequent administration, are believed to be within the skill of those in the art.

- 37 -

**A. Therapeutic Considerations:** In general, for therapeutic applications, a patient (i.e., an animal, including a human, having or predisposed to a disease or disorder) is administered one or more oligonucleotides, in accordance with the invention in a pharmaceutically acceptable carrier in doses ranging from 0.01 µg to 100 g per kg of body weight depending on the age of the patient and the severity of the disorder or disease state being treated. Further, the treatment regimen may last for a period of time which will vary depending upon the nature of the particular disease or disorder, its severity and the overall condition of the patient, and may extend from once daily to once every 20 years. In the context of the invention, the term "treatment regimen" is meant to encompass therapeutic, palliative and prophylactic modalities. Following treatment, the patient is monitored for changes in his/her condition and for alleviation of the symptoms of the disorder or disease state. The dosage of the nucleic acid may either be increased in the event the patient does not respond significantly to current dosage levels, or the dose may be decreased if an alleviation of the symptoms of the disorder or disease state is observed, or if the disorder or disease state has been ablated.

Dosing is dependent on severity and responsiveness of the disease state to be treated, with the course of treatment lasting from several days to several months, or until a cure is effected or a diminution of the disease state is achieved. Optimal dosing schedules can be calculated from measurements of drug accumulation in the body of the patient. Persons of ordinary skill can easily determine optimum dosages, dosing methodologies and repetition rates. Optimum dosages may vary depending on the relative potency of individual oligonucleotides, and

can generally be estimated based on EC<sub>50</sub>s found to be effective in *in vitro* and *in vivo* animal models. In general, dosage is from 0.01 µg to 100 g per kg of body weight, and may be given once or more daily, weekly, 5 monthly or yearly, or even once every 2 to 20 years. An optimal dosing schedule is used to deliver a therapeutically effective amount of the oligonucleotide being administered via a particular mode of administration.

The term "therapeutically effective amount," for the 10 purposes of the invention, refers to the amount of oligonucleotide-containing pharmaceutical composition which is effective to achieve an intended purpose without undesirable side effects (such as toxicity, irritation or allergic response). Although individual needs may vary, 15 determination of optimal ranges for effective amounts of pharmaceutical compositions is within the skill of the art. Human doses can be extrapolated from animal studies (Katocs et al., Chapter 27 *In: Remington's Pharmaceutical Sciences*, 18th Ed., Gennaro, ed., Mack Publishing Co., Easton, PA, 20 1990). Generally, the dosage required to provide an effective amount of a pharmaceutical composition, which can be adjusted by one skilled in the art, will vary depending on the age, health, physical condition, weight, type and extent of the disease or disorder of the recipient, 25 frequency of treatment, the nature of concurrent therapy (if any) and the nature and scope of the desired effect(s) (Nies et al., Chapter 3 *In: Goodman & Gilman's The Pharmacological Basis of Therapeutics*, 9th Ed., Hardman et al., eds., McGraw-Hill, New York, NY, 1996).

30 As used herein, the term "high risk individual" is meant to refer to an individual for whom it has been determined, via, e.g., individual or family history or genetic testing, has a significantly higher than normal

probability of being susceptible to the onset or recurrence of a disease or disorder. As part of treatment regimen for a high risk individual, the individual can be prophylactically treated to prevent the onset or recurrence 5 of the disease or disorder. The term "prophylactically effective amount" is meant to refer to an amount of a pharmaceutical composition which produces an effect observed as the prevention of the onset or recurrence of a disease or disorder. Prophylactically effective amounts of 10 a pharmaceutical composition are typically determined by the effect they have compared to the effect observed when a second pharmaceutical composition lacking the active agent is administered to a similarly situated individual.

Following successful treatment, it may be desirable 15 to have the patient undergo maintenance therapy to prevent the recurrence of the disease state, wherein the nucleic acid is administered in maintenance doses, ranging from 0.01 µg to 100 g per kg of body weight, once or more daily, to once every 20 years. For example, in the case of in 20 individual known or suspected of being prone to an autoimmune or inflammatory condition, prophylactic effects may be achieved by administration of preventative doses, ranging from 0.01 µg to 100 g per kg of body weight, once or more daily, to once every 20 years. In like fashion, an 25 individual may be made less susceptible to an inflammatory condition that is expected to occur as a result of some medical treatment, e.g., graft versus host disease resulting from the transplantation of cells, tissue or an organ into the individual.

30 In some cases it may be more effective to treat a patient with an oligonucleotide of the invention in conjunction with other traditional therapeutic modalities in order to increase the efficacy of a treatment regimen.

- 40 -

In the context of the invention, the term "treatment regimen" is meant to encompass therapeutic, palliative and prophylactic modalities. For example, a patient may be treated with conventional chemotherapeutic agents,

5 particularly those used for tumor and cancer treatment. Examples of such chemotherapeutic agents include but are not limited to daunorubicin, daunomycin, dactinomycin, doxorubicin, epirubicin, idarubicin, esorubicin, bleomycin, mafosfamide, ifosfamide, cytosine arabinoside, bis-

10 chloroethylnitrosurea, busulfan, mitomycin C, actinomycin D, mithramycin, prednisone, hydroxyprogesterone, testosterone, tamoxifen, dacarbazine, procarbazine, hexamethylmelamine, pentamethylmelamine, mitoxantrone, amsacrine, chlorambucil, methylcyclohexylnitrosurea,

15 nitrogen mustards, melphalan, cyclophosphamide, 6-mercaptopurine, 6-thioguanine, cytarabine (CA), 5-azacytidine, hydroxyurea, deoxycoformycin, 4-hydroxyperoxycyclophosphoramide, 5-fluorouracil (5-FU), 5-fluorodeoxyuridine (5-FUDR), methotrexate (MTX),

20 colchicine, vincristine, vinblastine, etoposide, trimetrexate, teniposide, cisplatin and diethylstilbestrol (DES). See, generally, *The Merck Manual of Diagnosis and Therapy*, 15th Ed., pp. 1206-1228, Berkow et al., eds., Rahay, N.J., 1987). When used with the compounds of the

25 invention, such chemotherapeutic agents may be used individually (e.g., 5-FU and oligonucleotide), sequentially (e.g., 5-FU and oligonucleotide for a period of time followed by MTX and oligonucleotide), or in combination with one or more other such chemotherapeutic agents (e.g.,

30 5-FU, MTX and oligonucleotide, or 5-FU, radiotherapy and oligonucleotide).

In another preferred embodiment of the invention, a first antisense oligonucleotide targeted to a first JNK

protein is used in combination with a second antisense oligonucleotide targeted to a second JNK protein in order to such JNK proteins to a more extensive degree than can be achieved when either oligonucleotide is used individually.

- 5 In various embodiments of the invention, the first and second JNK proteins which are targeted by such oligonucleotides are identical, are different JNK proteins or are different isoforms of the same JNK protein.

**B. Pharmaceutical Compositions:** Pharmaceutical

- 10 compositions for the non-parenteral administration of oligonucleotides may include sterile aqueous solutions which may also contain buffers, diluents and other suitable additives. Pharmaceutically acceptable organic or inorganic carrier substances suitable for non-parenteral  
15 administration which do not deleteriously react with oligonucleotides can be used. Suitable pharmaceutically acceptable carriers include, but are not limited to, water, salt solutions, alcohol, polyethylene glycols, gelatin, lactose, amylose, magnesium stearate, talc, silicic acid,  
20 viscous paraffin, hydroxymethylcellulose, polyvinylpyrrolidone and the like. The pharmaceutical compositions can be sterilized and, if desired, mixed with auxiliary agents, e.g., lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for  
25 influencing osmotic pressure, buffers, colorings flavorings and/or aromatic substances and the like which do not deleteriously react with the oligonucleotide(s) of the pharmaceutical composition. Pharmaceutical compositions in the form of aqueous suspensions may contain substances  
30 which increase the viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol and/or dextran. Optionally, such suspensions may also contain stabilizers.

- 42 -

In one embodiment of the invention, an oligonucleotide is administered via the rectal mode. In particular, pharmaceutical compositions for rectal administration include foams, solutions (enemas) and 5 suppositories. Rectal suppositories for adults are usually tapered at one or both ends and typically weigh about 2 g each, with infant rectal suppositories typically weighing about one-half as much, when the usual base, cocoa butter, is used (Block, Chapter 87 *In: Remington's Pharmaceutical 10 Sciences*, 18th Ed., Gennaro, ed., Mack Publishing Co., Easton, PA, 1990).

In a preferred embodiment of the invention, one or more oligonucleotides are administered via oral delivery. Pharmaceutical compositions for oral administration include 15 powders or granules, suspensions or solutions in water or non-aqueous media, capsules, sachets, troches, tablets or SECs (soft elastic capsules or "caplets"). Thickeners, flavoring agents, diluents, emulsifiers, dispersing aids, carrier substances or binders may be desirably added to 20 such pharmaceutical compositions. The use of such pharmaceutical compositions has the effect of delivering the oligonucleotide to the alimentary canal for exposure to the mucosa thereof. Accordingly, the pharmaceutical composition can comprise material effective in protecting 25 the oligonucleotide from pH extremes of the stomach, or in releasing the oligonucleotide over time, to optimize the delivery thereof to a particular mucosal site. Enteric coatings for acid-resistant tablets, capsules and caplets are known in the art and typically include acetate 30 phthalate, propylene glycol and sorbitan monoleate.

Various methods for producing pharmaceutical compositions for alimentary delivery are well known in the art. See, generally, Nairn, Chapter 83; Block, Chapter 87;

Rudnic et al., Chapter 89; Porter, Chapter 90; and Longer et al., Chapter 91 In: *Remington's Pharmaceutical Sciences*, 18th Ed., Gennaro, ed., Mack Publishing Co., Easton, PA, 1990. The oligonucleotides of the invention can be

5 incorporated in a known manner into customary pharmaceutical compositions, such as tablets, coated tablets, pills, granules, aerosols, syrups, emulsions, suspensions and solutions, using inert, non-toxic, pharmaceutically acceptable carriers (excipients). The

10 therapeutically active compound should in each case be present here in a concentration of about 0.5% to about 95% by weight of the total mixture, i.e., in amounts which are sufficient to achieve the stated dosage range. The pharmaceutical compositions are prepared, for example, by

15 diluting the active compounds with pharmaceutically acceptable carriers, if appropriate using emulsifying agents and/or dispersing agents, and, for example, in the case where water is used as the diluent, organic solvents can be used as auxiliary solvents if appropriate.

20 Pharmaceutical compositions may be formulated in a conventional manner using additional pharmaceutically acceptable carriers as appropriate. Thus, the compositions may be prepared by conventional means with additional excipients such as binding agents (e.g., pregelatinised

25 maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (e.g., lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (e.g., magnesium stearate, talc or silica); disintegrates (e.g., starch or sodium starch glycolate); or wetting agents

30 (e.g., sodium lauryl sulfate). Tablets may be coated by methods well known in the art. The preparations may also contain flavoring, coloring and/or sweetening agents as appropriate.

The pharmaceutical compositions, which may conveniently be presented in unit dosage form, may be prepared according to conventional techniques well known in the pharmaceutical industry. Such techniques include the 5 step of bringing into association the active ingredient(s) with the pharmaceutically acceptable carrier(s). In general the pharmaceutical compositions are prepared by uniformly and intimately bringing into association the active ingredient(s) with liquid excipients or finely 10 divided solid excipients or both, and then, if necessary, shaping the product.

Pharmaceutical compositions of the present invention suitable for oral administration may be presented as discrete units such as capsules, cachets or tablets each 15 containing predetermined amounts of the active ingredients; as powders or granules; as solutions or suspensions in an aqueous liquid or a non-aqueous liquid; or as oil-in-water emulsions or water-in-oil liquid emulsions. A tablet may be made by compression or molding, optionally with one or 20 more accessory ingredients. Compressed tablets may be prepared by compressing in a suitable machine, the active ingredients in a free-flowing form such as a powder or granules, optionally mixed with a binder, lubricant, inert diluent, preservative, surface active or dispersing agent. 25 Molded tablets may be made by molding in a suitable machine a mixture of the powdered compound moistened with an inert liquid diluent. The tablets may optionally be coated or scored and may be formulated so as to provide slow or controlled release of the active ingredients therein. 30 Pharmaceutical compositions for parenteral, intrathecal or intraventricular administration, or colloidal dispersion systems, may include sterile aqueous solutions which may also contain buffers, diluents and other suitable additives.

C. Penetration Enhancers: Pharmaceutical compositions comprising the oligonucleotides of the present invention may also include penetration enhancers in order to enhance the alimentary delivery of the oligonucleotides.

5 Penetration enhancers may be classified as belonging to one of five broad categories, i.e., fatty acids, bile salts, chelating agents, surfactants and non-surfactants (Lee et al., *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, 8:91-192; Muranishi, *Critical Reviews in Therapeutic*

10 *Drug Carrier Systems*, 1990, 7:1).

1. Fatty Acids: Various fatty acids and their derivatives which act as penetration enhancers include, for example, oleic acid, lauric acid, capric acid, myristic acid, palmitic acid, stearic acid, linoleic acid, 15 linolenic acid, dicaprate, tricaprate, recinleate, monoolein (a.k.a. 1-monooleoyl-rac-glycerol), dilaurin, caprylic acid, arachidonic acid, glyceryl 1-monocaprate, 1-dodecylazacycloheptan-2-one, acylcarnitines, acylcholines, mono- and di-glycerides and physiologically acceptable 20 salts thereof (i.e., oleate, laurate, caprate, myristate, palmitate, stearate, linoleate, etc.) (Lee et al., *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, page 92; Muranishi, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1990, 7:1; El-Hariri et al., *J. Pharm. Pharmacol.*, 25 1992, 44:651).

2. Bile Salts: The physiological roles of bile include the facilitation of dispersion and absorption of lipids and fat-soluble vitamins (Brunton, Chapter 38 In: *Goodman & Gilman's The Pharmacological Basis of Therapeutics*, 9th Ed., Hardman et al., eds., McGraw-Hill, New York, NY, 1996, pages 934-935). Various natural bile salts, and their synthetic derivatives, act as penetration enhancers. Thus, the term "bile salt" includes any of the

- 46 -

naturally occurring components of bile as well as any of their synthetic derivatives.

**3. Chelating Agents:** Chelating agents have the added advantage of also serving as DNase inhibitors and 5 include, but are not limited to, disodium ethylenediaminetetraacetate (EDTA), citric acid, salicylates (e.g., sodium salicylate, 5-methoxysalicylate and homovanilate), N-acyl derivatives of collagen, laureth-9 and N-amino acyl derivatives of beta-diketones 10 (enamines) (Lee et al., *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, page 92; Muranishi, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1990, 7:1; Buur et al., *J. Control Rel.*, 1990, 14:43).

**4. Surfactants:** Surfactants include, for 15 example, sodium lauryl sulfate, polyoxyethylene-9-lauryl ether and polyoxyethylene-20-cetyl ether (Lee et al., *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, page 92); and perfluorochemical emulsions, such as FC-43 (Takahashi et al., *J. Pharm. Pharmacol.*, 1988, 40:252).

20 **5. Non-Surfactants:** Non-surfactants include, for example, unsaturated cyclic ureas, 1-alkyl- and 1-alkenylazacyclo-alkanone derivatives (Lee et al., *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, page 92); and non-steroidal anti-inflammatory agents such 25 as diclofenac sodium, indomethacin and phenylbutazone (Yamashita et al., *J. Pharm. Pharmacol.*, 1987, 39:621).

**D. Carrier Compounds:** As used herein, "carrier compound" refers to a nucleic acid, or analog thereof, which is inert (i.e., does not possess biological activity 30 *per se*) but is recognized as a nucleic acid by *in vivo* processes that reduce the bioavailability of a nucleic acid having biological activity by, for example, degrading the biologically active nucleic acid or promoting its removal

- 47 -

from circulation. The coadministration of a nucleic acid and a carrier compound, typically with an excess of the latter substance, can result in a substantial reduction of the amount of nucleic acid recovered in the liver, kidney or other extracirculatory reservoirs, presumably due to competition between the carrier compound and the nucleic acid for a common receptor. For example, the recovery of a partially phosphorothioated oligonucleotide in hepatic tissue is reduced when it is coadministered with polyinosinic acid, dextran sulfate, polycytidic acid or 4-acetamido-4'-isothiocyanostilbene-2,2'-disulfonic acid (Miyao et al., *Antisense Res. Dev.*, 1995, 5:115; Takakura et al., *Antisense & Nucl. Acid Drug Dev.*, 1996, 6:177).

**E. Pharmaceutically Acceptable Carriers:** In

contrast to a carrier compound, a "pharmaceutically acceptable carrier" (excipient) is a pharmaceutically acceptable solvent, suspending agent or any other pharmacologically inert vehicle for delivering one or more nucleic acids to an animal. The pharmaceutically acceptable carrier may be liquid or solid and is selected with the planned manner of administration in mind so as to provide for the desired bulk, consistency, etc., when combined with a nucleic acid and the other components of a given pharmaceutical composition. Typical pharmaceutically acceptable carriers include, but are not limited to, binding agents (e.g., pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose, etc.); fillers (e.g., lactose and other sugars, microcrystalline cellulose, pectin, gelatin, calcium sulfate, ethyl cellulose, polyacrylates or calcium hydrogen phosphate, etc.); lubricants (e.g., magnesium stearate, talc, silica, colloidal silicon dioxide, stearic acid, metallic stearates, hydrogenated vegetable oils, corn

starch, polyethylene glycols, sodium benzoate, sodium acetate, etc.); disintegrates (e.g., starch, sodium starch glycolate, etc.); or wetting agents (e.g., sodium lauryl sulphate, etc.). Sustained release oral delivery systems and/or enteric coatings for orally administered dosage forms are described in U.S. Patents Nos. 4,704,295; 4,556,552; 4,309,406; and 4,309,404.

**F. Miscellaneous Additional Components:** The compositions of the present invention may additionally contain other adjunct components conventionally found in pharmaceutical compositions, at their art-established usage levels. Thus, for example, the compositions may contain additional compatible pharmaceutically-active materials such as, e.g., antipruritics, astringents, local anesthetics or anti-inflammatory agents, or may contain additional materials useful in physically formulating various dosage forms of the composition of present invention, such as dyes, flavoring agents, preservatives, antioxidants, opacifiers, thickening agents and stabilizers. However, such materials, when added, should not unduly interfere with the biological activities of the components of the compositions of the invention.

**G. Colloidal Dispersion Systems:** Regardless of the method by which the oligonucleotides of the invention are introduced into a patient, colloidal dispersion systems may be used as delivery vehicles to enhance the *in vivo* stability of the oligonucleotides and/or to target the oligonucleotides to a particular organ, tissue or cell type. Colloidal dispersion systems include, but are not limited to, macromolecule complexes, nanocapsules, microspheres, beads and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles and liposomes. A preferred colloidal dispersion system is a plurality of

liposomes, artificial membrane vesicles which may be used as cellular delivery vehicles for bioactive agents *in vitro* and *in vivo* (Mannino et al., *Biotechniques*, 1988, 6, 682; Blume and Cevc, *Biochem. et Biophys. Acta*, 1990, 1029, 91; 5 Lappalainen et al., *Antiviral Res.*, 1994, 23, 119; Chonn and Cullis, *Current Op. Biotech.*, 1995, 6, 698). It has been shown that large unilamellar vesicles (LUV), which range in size from 0.2-0.4 µm, can encapsulate a substantial percentage of an aqueous buffer containing 10 large macromolecules. RNA, DNA and intact virions can be encapsulated within the aqueous interior and delivered to brain cells in a biologically active form (Fraley et al., *Trends Biochem. Sci.*, 1981, 6, 77). The composition of the liposome is usually a combination of lipids, particularly 15 phospholipids, in particular, high phase transition temperature phospholipids, usually in combination with one or more steroids, particularly cholesterol. Examples of lipids useful in liposome production include phosphatidyl compounds, such as phosphatidylglycerol, 20 phosphatidylcholine, phosphatidylserine, sphingolipids, phosphatidylethanolamine, cerebrosides and gangliosides. Particularly useful are diacyl phosphatidylglycerols, where the lipid moiety contains from 14-18 carbon atoms, particularly from 16-18 carbon atoms, and is saturated 25 (lacking double bonds within the 14-18 carbon atom chain). Illustrative phospholipids include phosphatidylcholine, dipalmitoylphosphatidylcholine and distearoylphosphatidylcholine.

The targeting of colloidal dispersion systems, 30 including liposomes, can be either passive or active. Passive targeting utilizes the natural tendency of liposomes to distribute to cells of the reticuloendothelial system in organs that contain sinusoidal capillaries.

- 50 -

Active targeting, by contrast, involves modification of the liposome by coupling thereto a specific ligand such as a viral protein coat (Morishita et al., *Proc. Natl. Acad. Sci. (U.S.A.)*, 1993, 90, 8474), monoclonal antibody (or a 5 suitable binding portion thereof), sugar, glycolipid or protein (or a suitable oligopeptide fragment thereof), or by changing the composition and/or size of the liposome in order to achieve distribution to organs and cell types other than the naturally occurring sites of localization.

10 The surface of the targeted colloidal dispersion system can be modified in a variety of ways. In the case of a liposomal targeted delivery system, lipid groups can be incorporated into the lipid bilayer of the liposome in order to maintain the targeting ligand in close association 15 with the lipid bilayer. Various linking groups can be used for joining the lipid chains to the targeting ligand. The targeting ligand, which binds a specific cell surface molecule found predominantly on cells to which delivery of the oligonucleotides of the invention is desired, may be, 20 for example, (1) a hormone, growth factor or a suitable oligopeptide fragment thereof which is bound by a specific cellular receptor predominantly expressed by cells to which delivery is desired or (2) a polyclonal or monoclonal antibody, or a suitable fragment thereof (e.g., Fab; 25 F(ab')<sub>2</sub>) which specifically binds an antigenic epitope found predominantly on targeted cells. Two or more bioactive agents (e.g., an oligonucleotide and a conventional drug; two oligonucleotides) can be combined within, and delivered by, a single liposome. It is also possible to add agents 30 to colloidal dispersion systems which enhance the intercellular stability and/or targeting of the contents thereof.

- 51 -

**5. Means of Administration:** The present invention provides compositions comprising oligonucleotides intended for administration to an animal. For purposes of the invention, unless otherwise specified, the term "animal" is 5 meant to encompass humans as well as other mammals, as well as reptiles, amphibians, and birds.

**A. Parenteral Delivery:** The term "parenteral delivery" refers to the administration of an oligonucleotide of the invention to an animal in a manner 10 other than through the digestive canal. Means of preparing and administering parenteral pharmaceutical compositions are known in the art (see, e.g., Avis, Chapter 84 In: *Remington's Pharmaceutical Sciences*, 18th Ed., Gennaro, ed., Mack Publishing Co., Easton, PA, 1990, pages 1545- 15 1569). Parenteral means of delivery include, but are not limited to, the following illustrative examples.

1. **Intravitreal injection**, for the direct delivery of drug to the vitreous humor of a mammalian eye, is described in U.S. Patent No. 5,591,720, the contents of 20 which are hereby incorporated by reference. Means of preparing and administering ophthalmic preparations are known in the art (see, e.g., Mullins et al., Chapter 86 In: *Remington's Pharmaceutical Sciences*, 18th Ed., Gennaro, ed., Mack Publishing Co., Easton, PA, 1990, pages 1581- 25 1595).

2. **Intravenous administration** of antisense oligonucleotides to various non-human mammals has been described by Iversen (Chapter 26 In: *Antisense Research and Applications*, Crooke et al., eds., CRC Press, Boca Raton, 30 FL, 1993, pages 461-469). Systemic delivery of oligonucleotides to non-human mammals via intraperitoneal means has also been described (Dean et al., *Proc. Natl. Acad. Sci. (U.S.A.)*, 1994, 91, 11766).

- 52 -

**3. Intraluminal drug administration,** for the direct delivery of drug to an isolated portion of a tubular organ or tissue (e.g., such as an artery, vein, ureter or urethra), may be desired for the treatment of 5 patients with diseases or conditions afflicting the lumen of such organs or tissues. To effect this mode of oligonucleotide administration, a catheter or cannula is surgically introduced by appropriate means. For example, for treatment of the left common carotid artery, a cannula 10 is inserted thereinto via the external carotid artery. After isolation of a portion of the tubular organ or tissue for which treatment is sought, a composition comprising the oligonucleotides of the invention is infused through the cannula or catheter into the isolated segment. After 15 incubation for from about 1 to about 120 minutes, during which the oligonucleotide is taken up by cells of the interior lumen of the vessel, the infusion cannula or catheter is removed and flow within the tubular organ or tissue is restored by removal of the ligatures which 20 effected the isolation of a segment thereof (Morishita et al., *Proc. Natl. Acad. Sci. U.S.A.*, 1993, 90, 8474). Antisense oligonucleotides may also be combined with a biocompatible matrix, such as a hydrogel material, and applied directly to vascular tissue *in vivo* (Rosenberg et 25 al., U.S. Patent No. 5,593,974, issued January 14, 1997).

**4. Intraventricular drug administration,** for the direct delivery of drug to the brain of a patient, may be desired for the treatment of patients with diseases or conditions afflicting the brain. To effect this mode of 30 oligonucleotide administration, a silicon catheter is surgically introduced into a ventricle of the brain of a human patient, and is connected to a subcutaneous infusion pump (Medtronic Inc., Minneapolis, MN) that has been

surgically implanted in the abdominal region (Zimm et al., *Cancer Research*, 1984, 44, 1698; Shaw, *Cancer*, 1993, 72(11 Suppl.), 3416). The pump is used to inject the oligonucleotides and allows precise dosage adjustments and  
5 variation in dosage schedules with the aid of an external programming device. The reservoir capacity of the pump is 18-20 mL and infusion rates may range from 0.1 mL/h to 1 mL/h. Depending on the frequency of administration, ranging from daily to monthly, and the dose of drug to be  
10 administered, ranging from 0.01 µg to 100 g per kg of body weight, the pump reservoir may be refilled at 3-10 week intervals. Refilling of the pump is accomplished by percutaneous puncture of the self-sealing septum of the pump.

15                 **5. Intrathecal drug administration**, for the introduction of a drug into the spinal column of a patient may be desired for the treatment of patients with diseases of the central nervous system. To effect this route of oligonucleotide administration, a silicon catheter is  
20 surgically implanted into the L3-4 lumbar spinal interspace of a human patient, and is connected to a subcutaneous infusion pump which has been surgically implanted in the upper abdominal region (Luer and Hatton, *The Annals of Pharmacotherapy*, 1993, 27, 912; Ettinger et al., 1978,  
25 *Cancer*, 41, 1270, 1978; Yaida et al., *Regul. Pept.*, 1995, 59, 193). The pump is used to inject the oligonucleotides and allows precise dosage adjustments and variations in dose schedules with the aid of an external programming device. The reservoir capacity of the pump is 18-20 mL,  
30 and infusion rates may vary from 0.1 mL/h to 1 mL/h. Depending on the frequency of drug administration, ranging from daily to monthly, and dosage of drug to be administered, ranging from 0.01 µg to 100 g per kg of body

- 54 -

weight, the pump reservoir may be refilled at 3-10 week intervals. Refilling of the pump is accomplished by a single percutaneous puncture to the self-sealing septum of the pump. The distribution, stability and pharmacokinetics 5 of oligonucleotides within the central nervous system may be followed according to known methods (Whitesell et al., *Proc. Natl. Acad. Sci. (USA)*, 1993, 90, 4665).

To effect delivery of oligonucleotides to areas other than the brain or spinal column via this method, the 10 silicon catheter is configured to connect the subcutaneous infusion pump to, e.g., the hepatic artery, for delivery to the liver (Kemeny et al., *Cancer*, 1993, 71, 1964). Infusion pumps may also be used to effect systemic delivery 15 of oligonucleotides (Ewel et al., *Cancer Research*, 1992, 52, 3005; Rubenstein et al., *J. Surg. Oncol.*, 1996, 62, 194).

**6. Epidermal and Transdermal Delivery**, in which pharmaceutical compositions containing drugs are applied topically, can be used to administer drugs to be 20 absorbed by the local dermis or for further penetration and absorption by underlying tissues, respectively. Means of preparing and administering medications topically are known in the art (see, e.g., Block, Chapter 87 *In: Remington's Pharmaceutical Sciences*, 18th Ed., Gennaro, ed., Mack 25 Publishing Co., Easton, PA, 1990, pages 1596-1609).

**7. Vaginal Delivery** provides local treatment and avoids first pass metabolism, degradation by digestive enzymes, and potential systemic side-effects. This mode of administration may be preferred for antisense 30 oligonucleotides targeted to pathogenic organisms for which the vagina is the usual habitat, e.g., *Trichomonas vaginalis*. In another embodiment, antisense oligonucleotides to genes encoding sperm-specific

antibodies can be delivered by this mode of administration in order to increase the probability of conception and subsequent pregnancy. Vaginal suppositories (Block, Chapter 87 In: *Remington's Pharmaceutical Sciences*, 18th 5 Ed., Gennaro, ed., Mack Publishing Co., Easton, PA, 1990, pages 1609-1614) or topical ointments can be used to effect this mode of delivery.

8. **Intravesical Delivery** provides local treatment and avoids first pass metabolism, degradation by 10 digestive enzymes, and potential systemic side-effects. However, the method requires urethral catheterization of the patient and a skilled staff. Nevertheless, this mode of administration may be preferred for antisense oligonucleotides targeted to pathogenic organisms, such as 15 *T. vaginalis*, which may invade the urogenital tract.

B. **Alimentary Delivery:** The term "alimentary delivery" refers to the administration, directly or otherwise, to a portion of the alimentary canal of an animal. The term "alimentary canal" refers to the tubular 20 passage in an animal that functions in the digestion and absorption of food and the elimination of food residue, which runs from the mouth to the anus, and any and all of its portions or segments, e.g., the oral cavity, the esophagus, the stomach, the small and large intestines and 25 the colon, as well as compound portions thereof such as, e.g., the gastro-intestinal tract. Thus, the term "alimentary delivery" encompasses several routes of administration including, but not limited to, oral, rectal, endoscopic and sublingual/buccal administration. A common 30 requirement for these modes of administration is absorption over some portion or all of the alimentary tract and a need for efficient mucosal penetration of the nucleic acid(s) so administered.

- 56 -

**1. Buccal/Sublingual Administration:**

Delivery of a drug via the oral mucosa has several desirable features, including, in many instances, a more rapid rise in plasma concentration of the drug than via 5 oral delivery (Harvey, Chapter 35 *In: Remington's Pharmaceutical Sciences*, 18th Ed., Gennaro, ed., Mack Publishing Co., Easton, PA, 1990, page 711). Furthermore, because venous drainage from the mouth is to the superior vena cava, this route also bypasses rapid first-pass 10 metabolism by the liver. Both of these features contribute to the sublingual route being the mode of choice for nitroglycerin (Benet et al., Chapter 1 *In: Goodman & Gilman's The Pharmacological Basis of Therapeutics*, 9th Ed., Hardman et al., eds., McGraw-Hill, New York, NY, 1996, 15 page 7).

**2. Endoscopic Administration:** Endoscopy

can be used for drug delivery directly to an interior portion of the alimentary tract. For example, endoscopic retrograde cystopancreatography (ERCP) takes advantage of 20 extended gastroscopy and permits selective access to the biliary tract and the pancreatic duct (Hirahata et al., *Gan To Kagaku Ryoho*, 1992, 19(10 Suppl.):1591). However, the procedure is unpleasant for the patient, and requires a highly skilled staff.

**25 3. Rectal Administration:** Drugs

administered by the oral route can often be alternatively administered by the lower enteral route, i.e., through the anal portal into the rectum or lower intestine. Rectal suppositories, retention enemas or rectal catheters can be 30 used for this purpose and may be preferred when patient compliance might otherwise be difficult to achieve (e.g., in pediatric and geriatric applications, or when the patient is vomiting or unconscious). Rectal administration

- 57 -

may result in more prompt and higher blood levels than the oral route, but the converse may be true as well (Harvey, Chapter 35 *In: Remington's Pharmaceutical Sciences*, 18th Ed., Gennaro, ed., Mack Publishing Co., Easton, PA, 1990, 5 page 711). Because about 50% of the drug that is absorbed from the rectum will bypass the liver, administration by this route significantly reduces the potential for first-pass metabolism (Benet et al., Chapter 1 *In: Goodman & Gilman's The Pharmacological Basis of Therapeutics*, 9th 10 Ed., Hardman et al., eds., McGraw-Hill, New York, NY, 1996).

**4. Oral Administration:** The preferred method of administration is oral delivery, which is typically the most convenient route for access to the 15 systemic circulation. Absorption from the alimentary canal is governed by factors that are generally applicable, e.g., surface area for absorption, blood flow to the site of absorption, the physical state of the drug and its concentration at the site of absorption (Benet et al., 20 Chapter 1 *In: Goodman & Gilman's The Pharmacological Basis of Therapeutics*, 9th Ed., Hardman et al., eds., McGraw-Hill, New York, NY, 1996, pages 5-7). A significant factor which may limit the oral bioavailability of a drug is the degree of "first pass effects." For example, some 25 substances have such a rapid hepatic uptake that only a fraction of the material absorbed enters the peripheral blood (Van Berge-Henegouwen et al., *Gastroenterology*, 1977, 73:300). The compositions and methods of the invention circumvent, at least partially, such first pass effects by 30 providing improved uptake of nucleic acids and thereby, e.g., causing the hepatic uptake system to become saturated and allowing a significant portion of the nucleic acid so administered to reach the peripheral circulation.

Additionally or alternatively, the hepatic uptake system is saturated with one or more inactive carrier compounds prior to administration of the active nucleic acid.

The following examples illustrate the invention and 5 are not intended to limit the same. Those skilled in the art will recognize, or be able to ascertain through routine experimentation, numerous equivalents to the specific substances and procedures described herein. Such equivalents are considered to be within the scope of the 10 present invention.

#### **EXAMPLES**

##### **Example 1: Synthesis of Oligonucleotides**

**A. General Synthetic Techniques:** Oligonucleotides were synthesized on an automated DNA synthesizer using 15 standard phosphoramidite chemistry with oxidation using iodine.  $\beta$ -Cyanoethyldiisopropyl phosphoramidites were purchased from Applied Biosystems (Foster City, CA). For phosphorothioate oligonucleotides, the standard oxidation bottle was replaced by a 0.2 M solution of 3H-1,2- 20 benzodithiole-3-one-1,1-dioxide in acetonitrile for the stepwise thiation of the phosphite linkages.

The synthesis of 2'-O-methyl- (a.k.a. 2'-methoxy-) phosphorothioate oligonucleotides is according to the procedures set forth above substituting 2'-O-methyl  $\beta$ - 25 cyanoethyldiisopropyl phosphoramidites (Chemgenes, Needham, MA) for standard phosphoramidites and increasing the wait cycle after the pulse delivery of tetrazole and base to 360 seconds.

Similarly, 2'-O-propyl- (a.k.a 2'-propoxy-) 30 phosphorothioate oligonucleotides are prepared by slight modifications of this procedure and essentially according to procedures disclosed in U.S. patent application Serial

- 59 -

No. 08/383,666, filed February 3, 1995, which is assigned to the same assignee as the instant application.

The 2'-fluoro-phosphorothioate oligonucleotides of the invention are synthesized using 5'-dimethoxytrityl-3'-phosphoramidites and prepared as disclosed in U.S. patent application Serial No. 08/383,666, filed February 3, 1995, and U.S. Patent 5,459,255, which issued October 8, 1996, both of which are assigned to the same assignee as the instant application. The 2'-fluoro-oligonucleotides were 10 prepared using phosphoramidite chemistry and a slight modification of the standard DNA synthesis protocol (i.e., deprotection was effected using methanolic ammonia at room temperature).

The 2'-methoxyethoxy oligonucleotides were 15 synthesized essentially according to the methods of Martin et al. (*Helv. Chim. Acta*, 1995, 78, 486). For ease of synthesis, the 3' nucleotide of the 2'-methoxyethoxy oligonucleotides was a deoxynucleotide, and 2'-O-CH<sub>2</sub>CH<sub>2</sub>OCH<sub>3</sub>-cytosines were 5-methyl cytosines, which were synthesized 20 according to the procedures described below.

PNA antisense analogs are prepared essentially as described in U.S. Patents Nos. 5,539,082 and 5,539,083, both of which (1) issued July 23, 1996, and (2) are assigned to the same assignee as the instant application.

25       **B. Purification:** After cleavage from the controlled pore glass column (Applied Biosystems) and deblocking in concentrated ammonium hydroxide at 55°C for 18 hours, the oligonucleotides were purified by precipitation twice out of 0.5 M NaCl with 2.5 volumes ethanol. Analytical gel 30 electrophoresis was accomplished in 20% acrylamide, 8 M urea, 45 mM Tris-borate buffer, pH 7.0.

Oligodeoxynucleotides and their phosphorothioate analogs

- 60 -

were judged from electrophoresis to be greater than 80% full length material.

**Example 2: Assays for Oligonucleotide-Mediated Inhibition  
of JNK mRNA Expression in Human Tumor Cells**

5       In order to evaluate the activity of potential JNK-modulating oligonucleotides, human lung carcinoma cell line A549 (American Type Culture Collection, Rockville, MD No. ATCC CCL-185) cells or other cell lines as indicated in the Examples, were grown and treated with oligonucleotides or  
10 control solutions as detailed below. After harvesting, cellular extracts were prepared and examined for specific JNK mRNA levels or JNK protein levels (i.e., Northern or Western assays, respectively). In all cases, "% expression" refers to the amount of JNK-specific signal in  
15 an oligonucleotide-treated cell relative to an untreated cell (or a cell treated with a control solution that lacks oligonucleotide), and "% inhibition" is calculated as

$$100\% - \% \text{ Expression} = \% \text{ Inhibition.}$$

**Northern Assays:** The mRNA expression of each JNK protein was determined by using a nucleic acid probe specifically hybridizable thereto. Nucleic acid probes specific for JNK1, JNK2 and JNK3 are described in Examples 3, 4 and 5, respectively. The probes were radiolabelled by means well known in the art (see, e.g., *Short Protocols in Molecular Biology*, 2nd Ed., Ausubel et al., eds., John Wiley & Sons, New York, 1992, pages 3-11 to 2-3-44 and 4-17 to 4-18; Ruth, Chapter 6 *In: Methods in Molecular Biology*, Vol. 26: *Protocols for Oligonucleotide Conjugates*, Agrawal, ed., Humana Press Inc., Totowa, NJ, 1994, pages 167-185; 20 and Chapter 10 *In: Molecular Cloning: A Laboratory Manual*, 2nd Ed., Sambrook et al., eds., pages 10.1-10.70). The blots were stripped and reprobed with a  $^{32}\text{P}$ -labeled

- 61 -

glyceraldehyde 3-phosphate dehydrogenase (G3PDH) probe (Clontech Laboratories, Inc., Palo Alto, CA) in order to confirm equal loading of RNA and to allow the levels of JNK transcripts to be normalized with regard to the G3PDH signals.

A549 cells were grown in T-75 flasks until 80-90% confluent. At this time, the cells were washed twice with 10 mL of media (DMEM), followed by the addition of 5 mL of DMEM containing 20 µg/mL of LIPOFECTIN™ (i.e., 1:1 (w/w) DOTMA/DOPE, Life Technologies, Gaithersburg, MD; DOTMA = N-[1-(2,3-dioleyoxy)propyl]-N,N,N-trimethylammonium chloride; DOPE = dioleoyl phosphatidylethanolamine). The oligonucleotides were added from a 10 µM stock solution to a final concentration of 400 nM, and the two solutions were mixed by swirling the flasks. As a control, cells were treated with LIPOFECTIN™ without oligonucleotide under the same conditions and for the same times as the oligonucleotide-treated samples. After 4 hours at 37°C, the medium was replaced with fresh DMEM containing 10% serum. The cells were allowed to recover for 18 hours. Total cellular RNA was then extracted in guanidinium, subject to gel electrophoresis and transferred to a filter according to techniques known in the art (see, e.g., Chapter 7 *In: Molecular Cloning: A Laboratory Manual*, 2nd Ed., Sambrook et al., eds., pages 7.1-7.87, and *Short Protocols in Molecular Biology*, 2nd Ed., Ausubel et al., eds., John Wiley & Sons, New York, 1992, pages 2-24 to 2-30 and 4-14 to 4-29). Filters were typically hybridized overnight to a probe specific for the particular JNK gene of interest in hybridization buffer (25 mM KPO<sub>4</sub>, pH 7.4; 5x SSC; 5x Denhardt's solution, 100 µg/ml Salmon sperm DNA and 50% formamide) (Alahari et al., *Nucl. Acids Res.*, 1993, 21, 4079). This was followed by two washes with 1x SSC,

- 62 -

0.1%SDS and two washes with 0.25x SSC, 0.1% SDS. Hybridizing bands were visualized by exposure to X-OMAT AR film and quantitated using a PHOSPHORIMAGER™ essentially according to the manufacturer's instructions (Molecular Dynamics, Sunnyvale, CA).

**Western Assays:** A549 cells were grown and treated with oligonucleotides as described above. Cells were lysed, and protein extracts were electrophoresed (SDS-PAGE) and transferred to nitrocellulose filters by means known in the art (see, e.g., Chapter 18 *In: Molecular Cloning: A Laboratory Manual*, 2nd Ed., Sambrook et al., eds., pages 18.34, 18.47-18.54 and 18.60-18.75)). The amount of each JNK protein was determined by using a primary antibody that specifically recognizes the appropriate JNK protein. The primary antibodies specific for each JNK protein are described in the appropriate Examples. The primary antibodies were detected by means well known in the art (see, e.g., *Short Protocols in Molecular Biology*, 2nd Ed., Ausubel et al., eds., John Wiley & Sons, New York, 1992, pages 10-33 to 10-35; and Chapter 18 *In: Molecular Cloning: A Laboratory Manual*, 2nd Ed., Sambrook et al., eds., pages 18.1-18.75 and 18.86-18.88) and quantitated using a PHOSPHORIMAGER™ essentially according to the manufacturer's instructions (Molecular Dynamics, Sunnyvale, CA).

Levels of JNK proteins can also be quantitated by measuring the level of their corresponding kinase activity. Such kinase assays can be done in gels *in situ* (Hibi et al., *Genes & Dev.*, 1993, 7, 2135) or after immunoprecipitation from cellular extracts (Derijard et al., *Cell*, 1994, 76, 1025). Substrates and/or kits for such assays are commercially available from, for example, Upstate Biotechnology, Inc. (Lake Placid, NY), New England

- 63 -

Biolabs, Inc., (Beverly, MA) and Calbiochem-Novabiochem Biosciences, Inc., (La Jolla, CA).

**Example 3: Oligonucleotide-Mediated Inhibition of JNK1 Expression**

5       **A. JNK1 oligonucleotide sequences:** Table 1 lists the nucleotide sequences of a set of oligonucleotides designed to specifically hybridize to JNK1 mRNAs and their corresponding ISIS and SEQ ID numbers. The nucleotide co-ordinates of the target gene, *JNK1*, and gene target regions 10 are also included. The nucleotide co-ordinates are derived from GenBank accession No. L26318, locus name "HUMJNK1" (see also Figure 1(A) of Derijard et al., *Cell*, 1994, 76, 1025). The abbreviations for gene target regions are as follows: 5'-UTR, 5' untranslated region; tIR, translation 15 initiation region; ORF, open reading frame; 3'-UTR, 3' untranslated region. The nucleotides of the oligonucleotides whose sequences are presented in Table 1 are connected by phosphorothioate linkages and are unmodified at the 2' position (i.e., 2'-deoxy). It should 20 be noted that the oligonucleotide target co-ordinate positions and gene target regions may vary within mRNAs encoding related isoforms of JNK1 (see subsection G, below).

In addition to hybridizing to human JNK1 mRNAs, the 25 full oligonucleotide sequences of ISIS Nos. 12548 (SEQ ID NO: 17) and 12551 (SEQ ID NO: 20) hybridize to the 5' ends of mRNAs from *Rattus norvegicus* that encode a stress-activated protein kinase named "p54 $\gamma$ " (Kyriakis et al., *Nature*, 1994, 369, 156). Specifically, ISIS 12548 (SEQ ID 30 NO: 17) hybridizes to bases 498-517 of GenBank accession No. L27129, locus name "RATSAPKD," and ISIS 12551 (SEQ ID NO: 20) hybridizes to bases 803-822 of the same sequence. These oligonucleotides are thus preferred embodiments of

- 64 -

the invention for investigating the role of the p54 $\gamma$  protein kinase in rat *in vitro*, i.e., in cultured cells or tissues derived from whole animals, or *in vivo*.

B. **JNK1-specific probes:** In initial screenings of a 5 set of oligonucleotides derived from the JNK1 sequence (Table 2) for biological activity, a cDNA clone of JNK1 (Derijard et al., *Cell*, 1994, 76, 1025) was radiolabeled and used as a JNK1-specific probe in Northern blots.

Alternatively, however, one or more of the oligonucleotides 10 of Table 1 is detectably labeled and used as a JNK1-specific probe.

TABLE 1  
Nucleotide Sequences of JNK1 Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE (5' -> 3')	SEQ		TARGET GENE ID NO:	NUCLEOTIDE CO-ORDINATES	GENE TARGET REGION
		ID	NO:			
5	ATT-CTT-TCC-ACT-CTT-CTA-TT	1		1062-1081		ORF
11978	CTC-CTC-CAA-GTC-CAT-AAC-TT	2		1094-1113		ORF
11979	CCC-GTA-TAA-CTC-CAT-TCT-TG	3		1119-1138		ORF
11980	CTG-TGC-TAA-AGG-AGA-GGG-CT	4		1142-1161		ORF
11981	ATG-ATG-GAT-GCT-GAG-AGC-CA	5		1178-1197		3'-UTR
11982	GTT-GAC-ATT-GAA-GAC-ACA-TC	6		1215-1234		3'-UTR
11983	CTG-TAT-CAG-AGG-CCA-AAG-TC	7		1241-1260		3'-UTR
11984	TGC-TGC-TTC-TAG-ACT-GCT-GT	8		1261-1280		3'-UTR
11985	AGT-CAT-CTA-CAG-CAG-CCC-AG	9		1290-1309		3'-UTR
11986	CCA-TCC-CTC-CCA-CCC-CCC-GA	10		1320-1339		3'-UTR
11987						

ISIS NO.	NUCLEOTIDE SEQUENCE (5' -> 3')	SEQ ID NO.:	TARGET NUCLEOTIDE CO-ORDINATES	GENE TARGET REGION
11988	ATC-AAT-GAC-TAA-CCG-ACT-CC	11	1340-1359	3'-UTR
11989	CAA-AAA-TAA-GAC-CAC-TGA-AT	12	1378-1397	3'-UTR
12463	CAC-GCT-TGC-TTC-TGC-TCA-TG	13	0018-0037	TIR
12464	CGG-CTT-AGC-TTC-TTG-ATT-GC	14	0175-0194	ORF
5	CCC-GCT-TGG-CAT-GAG-TCT-GA	15	0207-0226	ORF
12539	CTC-TCT-GTA-GGC-CCG-CTT-GG	16	0218-0237	ORF
12548	ATT-TGC-ATC-CAT-GAG-CTC-CA	17	0341-0360	ORF
12549	CGT-TCC-TGC-AGT-CCT-GGC-CA	18	0533-0552	ORF
12550	GGA-TGA-CCT-CGG-GTG-CTC-TG	19	0591-0610	ORF
12551	CCC-ATA-ATG-CAC-CCC-ACA-GA	20	0646-0665	ORF
12552	CGG-GTG-TTG-GAG-AGC-TTC-AT	21	0956-0975	ORF
12553	TTT-GGT-GGT-GGA-GCT-TCT-GC	22	1006-1025	ORF
12554	GGC-TGC-CCC-CGT-ATA-ACT-CC	23	1126-1145	ORF

- 67 -

ISIS NO.	NUCLEOTIDE SEQUENCE (5' -> 3')	SEQ ID NO:	TARGET NUCLEOTIDE CO-ORDINATES	GENE TARGET REGION
12555	TGC-TAA-AGG-AGA-GGG-CTG-CC	24	1139-1158	ORF
12556	AGG-CCA-AAG-TCG-GAT-CTG-TT	25	1232-1251	3'-UTR
12557	CCA-CCC-CCC-GAT-GGC-CCA-AG	26	1311-1330	3'-UTR

**C. Activities of JNK1 oligonucleotides:** The data from screening a set of JNK1-specific phosphorothioate oligonucleotides (Table 2) indicate the following results. Oligonucleotides showing activity in this assay, as 5 reflected by levels of inhibition from  $\geq$  about 50% to about 100% of JNK1 mRNA levels, include ISIS Nos. 11982, 11983, 12463, 12464, 12538, 12539, 12548, 12549, 12550, 12552, 12553, 12554, 12555, 12556 and 12557 (SEQ ID NOS: 5, 6, 13, 14, 15, 16, 17, 18, 19, 21, 22, 23, 24, 25 and 26, 10 respectively). These oligonucleotides are thus preferred embodiments of the invention for modulating JNK1 expression. Oligonucleotides showing levels of inhibition of from  $\geq$  about 80% to about 100% of JNK1 mRNAs in this assay, include ISIS Nos. 11982, 12539, 12548, 12554 and 15 12464 (SEQ ID NOS: 5, 16, 17 and 23, respectively). These oligonucleotides are thus more preferred embodiments of the invention for modulating JNK1 expression.

The time course of inhibition of JNK1 mRNA expression by ISIS 12539 (SEQ ID NO: 16) is shown in Table 3. 20 Following the 4 hour treatment with ISIS 12539, the level of inhibition of JNK1 was greater than about 85% ( $t=0$  h), rose to about 95% inhibition at  $t=4$  h, and subsequently remained at greater than or equal to about 80% ( $t=12$  and 48 h) or 60% ( $t=72$  h).

- 69 -

**TABLE 2**  
**Activities of JNK1 Oligonucleotides**

	<b>ISIS No:</b>	<b>SEQ ID NO:</b>	<b>GENE TARGET REGION</b>	<b>% EXPRESSION:</b>	<b>% INHIBITION:</b>
5	11978	1	ORF	85%	15%
	11979	2	ORF	90%	10%
	11980	3	ORF	85%	15%
	11981	4	ORF	62%	28%
	11982	5	3'-UTR	13%	87%
10	11983	6	3'-UTR	40%	60%
	11984	7	3'-UTR	53%	47%
	11985	8	3'-UTR	47%	53%
	11985	9	3'-UTR	90%	10%
	11987	10	3'-UTR	47%	53%
15	11988	11	3'-UTR	78%	22%
	11989	12	3'-UTR	60%	40%
	12463	13	tIR	23%	77%

- 70 -

ISIS No:	SEQ ID NO:	GENE TARGET REGION	% EXPRESSION:	% INHIBITION:
12464	14	ORF	18%	82%
12538	15	ORF	33%	67%
12539	16	ORF	9%	91%
12548	17	ORF	5%	95%
5	12549	ORF	28%	72%
	12550	ORF	40%	60%
	12551	ORF	52%	48%
	12552	ORF	34%	66%
	12553	ORF	25%	75%
10	12554	ORF	11%	89%
	12555	ORF	27%	73%
	12556	3'-UTR	41%	59%
	12557	3'-UTR	29%	71%

- 71 -

TABLE 3

**Time Course of Response to JNK1 Antisense  
Oligonucleotides (ASOs)**

ISIS #	SEQ ID NO:	ASO Description	Time	Normalized % Control	% Inhibition
<hr/>					
5	control	---	(LIPOFECTIN™ only)	0 h	100.0
	control	---	"	4 h	100.0
	control	---	"	12 h	100.0
	control	---	"	48 h	100.0
	control	---	"	72 h	100.0
<hr/>					
10	12539	16	JNK1 active	0 h	14.1
	12539	16	"	4 h	5.9
	12539	16	"	12 h	11.6
	12539	16	"	48 h	21.0
	12539	16	"	272 h	41.5
					58.5

15           **D. Additional JNK1 oligonucleotides:** The results for JNK1-specific oligonucleotides (Table 2) indicate that one of the most active phosphorothioate oligonucleotides for modulating JNK1 expression is ISIS 12539 (SEQ ID NO: 16). As detailed in Table 4, additional oligonucleotides based 20 on this oligonucleotide were designed to confirm and extend the findings described above.

               Oligonucleotides ISIS Nos. 14320 (SEQ ID NO: 27) and 14321 (SEQ ID NO: 28) are 2'-deoxy-phosphorothioate sense

- 72 -

strand and scrambled controls for ISIS 12539 (SEQ ID NO: 16), respectively. ISIS Nos. 15346 and 15347 are "gapmers" corresponding to ISIS 12539; both have 2'-methoxyethoxy "wings" (having phosphorothioate linkages in the case of 5 ISIS 15346 and phosphodiester linkages in the case of ISIS 15347) and a central 2'-deoxy "gap" designed to support RNaseH activity on the target mRNA molecule. Similarly, ISIS Nos. 15348 to 15350 are "wingmers" corresponding to ISIS 12539 and have a 5' or 3' 2'-methoxyethoxy RNaseH- 10 refractory "wing" and a 3' or 5' (respectively) 2'-deoxy "wing" designed to support RNaseH activity on the target *JNK1* mRNA.

The chemically modified derivatives of ISIS 12539 (SEQ ID NO: 16) were tested in the Northern assay described 15 herein at concentrations of 100 and 400 nM, and the data (Table 5) indicate the following results. At 400 nM, relative to the 2'-unmodified oligonucleotide ISIS 12539, both "gapmers" (ISIS Nos. 15346 and 15347) effected inhibition of *JNK1* mRNA expression up to at least about 88% 20 inhibition. Similarly, the four "wingmers" (ISIS Nos. 15348 to 15351) effected inhibition of *JNK1* expression of up to at least about 60 to 70% inhibition.

- 73 -

**TABLE 4**  
**Chemically Modified JNK1 Oligonucleotides**

ISIS NO.	NUCLEOTIDE SEQUENCE (5' -> 3') AND CHEMICAL MODIFICATIONS*	SEQ ID NO:	COMMENTS
5	C <sup>S</sup> T <sup>S</sup> C <sup>S</sup> T <sup>S</sup> G <sup>S</sup> T <sup>S</sup> A <sup>S</sup> G <sup>S</sup> G <sup>S</sup> C <sup>S</sup> C <sup>S</sup> C <sup>S</sup> G <sup>S</sup> C <sup>S</sup> T <sup>S</sup> T <sup>S</sup> G <sup>S</sup> G	16	active
	C <sup>S</sup> C <sup>S</sup> A <sup>S</sup> G <sup>S</sup> C <sup>S</sup> G <sup>S</sup> G <sup>S</sup> C <sup>S</sup> C <sup>S</sup> T <sup>S</sup> A <sup>S</sup> C <sup>S</sup> A <sup>S</sup> G <sup>S</sup> A <sup>S</sup> G <sup>S</sup> A <sup>S</sup> G	27	12539 sense control
	C <sup>S</sup> T <sup>S</sup> T <sup>S</sup> C <sup>S</sup> C <sup>S</sup> G <sup>S</sup> T <sup>S</sup> T <sup>S</sup> G <sup>S</sup> G <sup>S</sup> A <sup>S</sup> C <sup>S</sup> C <sup>S</sup> C <sup>S</sup> C <sup>S</sup> T <sup>S</sup> G <sup>S</sup> G <sup>S</sup> G	28	scrambled control
	C <sup>S</sup> T <sup>S</sup> C <sup>S</sup> T <sup>S</sup> C <sup>S</sup> T <sup>S</sup> G <sup>S</sup> T <sup>S</sup> A <sup>S</sup> G <sup>S</sup> G <sup>S</sup> C <sup>S</sup> C <sup>S</sup> C <sup>S</sup> G <sup>S</sup> C <sup>S</sup> T <sup>S</sup> T <sup>S</sup> G <sup>S</sup> G	16	fully 2'- methoxy- ethoxy
10	C <sup>S</sup> T <sup>S</sup> C <sup>S</sup> T <sup>S</sup> C <sup>S</sup> T <sup>S</sup> G <sup>S</sup> T <sup>S</sup> A <sup>S</sup> G <sup>S</sup> G <sup>S</sup> C <sup>S</sup> C <sup>S</sup> C <sup>S</sup> G <sup>S</sup> C <sup>S</sup> T <sup>S</sup> T <sup>S</sup> G <sup>S</sup> G	16	"gapmer"
	C <sup>O</sup> T <sup>O</sup> C <sup>O</sup> T <sup>O</sup> C <sup>S</sup> T <sup>S</sup> G <sup>S</sup> T <sup>S</sup> A <sup>S</sup> G <sup>S</sup> G <sup>S</sup> C <sup>S</sup> C <sup>S</sup> C <sup>S</sup> G <sup>S</sup> C <sup>O</sup> T <sup>O</sup> T <sup>O</sup> G <sup>O</sup> G	16	"gapmer"
	C <sup>S</sup> T <sup>S</sup> C <sup>S</sup> T <sup>S</sup> C <sup>S</sup> T <sup>S</sup> G <sup>S</sup> T <sup>S</sup> A <sup>S</sup> G <sup>S</sup> G <sup>S</sup> C <sup>S</sup> C <sup>S</sup> C <sup>S</sup> G <sup>S</sup> C <sup>S</sup> T <sup>S</sup> T <sup>S</sup> G <sup>S</sup> G	16	"wingmer"
	C <sup>S</sup> T <sup>S</sup> C <sup>S</sup> T <sup>S</sup> C <sup>S</sup> T <sup>S</sup> G <sup>S</sup> T <sup>S</sup> A <sup>S</sup> G <sup>S</sup> G <sup>S</sup> C <sup>S</sup> C <sup>S</sup> C <sup>S</sup> G <sup>S</sup> C <sup>S</sup> T <sup>S</sup> T <sup>S</sup> G <sup>S</sup> G	16	"wingmer"
15	C <sup>O</sup> T <sup>O</sup> C <sup>O</sup> T <sup>O</sup> C <sup>O</sup> T <sup>O</sup> G <sup>O</sup> T <sup>O</sup> A <sup>O</sup> G <sup>O</sup> G <sup>S</sup> C <sup>S</sup> C <sup>S</sup> C <sup>S</sup> G <sup>S</sup> C <sup>S</sup> T <sup>S</sup> T <sup>S</sup> G <sup>S</sup> G	16	"wingmer"
	C <sup>S</sup> T <sup>S</sup> C <sup>S</sup> T <sup>S</sup> C <sup>S</sup> T <sup>S</sup> G <sup>S</sup> T <sup>S</sup> A <sup>S</sup> G <sup>O</sup> G <sup>O</sup> C <sup>O</sup> C <sup>O</sup> G <sup>O</sup> C <sup>O</sup> T <sup>O</sup> T <sup>O</sup> G <sup>O</sup> G	16	"wingmer"
	C <sup>S</sup> T <sup>S</sup> C <sup>S</sup> T <sup>S</sup> C <sup>S</sup> T <sup>S</sup> G <sup>S</sup> T <sup>S</sup> A <sup>S</sup> G <sup>S</sup> G <sup>S</sup> <u>C</u> <sup>S</sup> <u>C</u> <sup>S</sup> <u>C</u> <sup>S</sup> G <sup>S</sup> C <sup>S</sup> T <sup>S</sup> T <sup>S</sup> G <sup>S</sup> G	1	fully 5- methyl- cytosine version of ISIS 15346

- 74 -

\*Emboldened residues, 2'-methoxyethoxy- residues (others are 2'-deoxy-) including "C" residues, 5-methyl-cytosines; "O", phosphodiester linkage; "S", phosphorothioate linkage.

--- "C" residues, 2'-deoxy 5-methylcytosine residues; ---

5

TABLE 5

**Activity of Chemically Modified JNK1 Antisense Oligonucleotides**

ISIS #	SEQ ID NO:	Oligonucleotide Description *	Dose	Normalized % Control
control	---	No oligonucleotide (LIPOFECTIN™ only)	----	100.0
10	12539	16	JNK1 active, fully P=S &	100 nM 56.4
	12539	16	fully 2'-deoxy	400 nM 26.7
15	15345	16	fully P=S & fully 2'-MOE	100 nM 95.4
	15345	16		400 nM 89.1
15	15346	16	gapmer: P=S, 2'-MOE wings;	100 nM 22.6
	15346	16	P=S, 2'-deoxy core	400 nM 11.0
15	15347	16	gapmer: P=O, 2'-MOE wings;	100 nM 27.1
	15347	16	P=S, 2-deoxy core	400 nM 11.7
20	15348	16	wingmer: fully P=S;	100 nM 30.4
	15348	16	5' 2'-MOE; 3' 2-deoxy	400 nM 32.9
20	15349	16	wingmer: fully P=S;	100 nM 42.5
	15349	16	5' 2-deoxy; 3' 2'-MOE	400 nM 35.5
	15351	16	wingmer: 5' P=O & 2'-MOE;	100 nM 45.1

- 75 -

15351	16	3' P=S & 2'-deoxy	400 nM	39.8
15350	16	wingmer: 5' P=S & 2'-	100 nM	71.1
15350	16	deoxy; 3' P=O & 2'-MOE	400 nM	41.3

\* Abbreviations: P=O, phosphodiester linkage; P=S, 5 phosphorothioate linkage; MOE, methoxyethoxy-.

**E. Dose- and sequence-dependent response to JNK1**

**oligonucleotides:** In order to demonstrate a dose-dependent response to ISIS 12539 (SEQ ID NO: 16), different concentrations (i.e., 50, 100, 200 and 400 nM) of ISIS 10 12539 were tested for their effect on JNK1 mRNA levels in A549 cells (Table 6). In addition, two control oligonucleotides (ISIS 14320, SEQ ID NO: 27, sense control, and ISIS 14321, SEQ ID NO: 28, scrambled control; see also Table 4) were also applied to A549 cells in order to 15 demonstrate the specificity of ISIS 12539. The results (Table 6) demonstrate that the response of A549 cells to ISIS 12539 is dependent on dose in an approximately linear fashion. In contrast, neither of the control oligonucleotides effect any consistent response on JNK1 20 mRNA levels.

**F. Western Assays:** In order to assess the effect of oligonucleotides targeted to JNK1 mRNAs on JNK1 protein levels, Western assays were performed essentially as described above in Example 2, with the following 25 exception(s) and/or modification(s). A primary antibody that specifically binds to JNK1 (catalog No. sc-474-G) was purchased from Santa Cruz Biotechnology, Inc. (Santa Cruz, CA; other JNK1-specific antibodies are available from StressGen Biotechnologies, Inc., Victoria, BC, Canada; and 30 Research Diagnostics, Inc., Flanders, NJ). In this experiment, cells were grown and treated with

- 76 -

oligonucleotide at 300 nM for the initial 20 hours and then at 200 nM for 4 hours. At t=48 h, aliquots were removed for Northern and Western analyses, and fresh media was added to the cells. Aliquots for analysis were also taken 5 at t=72 h. The samples from t=48 h and t=72 h were analyzed using the Northern and Western assays described above.

**TABLE 6**

**Dose-Dependent Responses to JNK1 Antisense Oligonucleotides**

	<b>ISIS #</b>	<b>SEQ ID NO:</b>	<b>Oligonucleotide Description</b>	<b>Dose</b>	<b>Normalized % Control</b>
10	control	---	No oligonucleotide (LIPOFECTIN™ only)	---	100.0
	12539	16	JNK1 active	50 nM	70.3
	12539	16	"	400 nM	51.6
	12539	16	"	200 nM	22.4
15	12539	16	"	400 nM	11.1
	14320	27	12539 sense control	50 nM	103.6
	14320	27	"	100 nM	76.3
	14320	27	"	200 nM	98.9
	14320	27	"	400 nM	97.1
20	14321	28	12539 scrambled control	50 nM	91.8
	14321	28	"	100 nM	94.1
	14321	28	"	200 nM	100.2
	14321	28	"	400 nM	79.2

- 77 -

The data (Table 7) indicate the following results.

In this assay, at t=48 h, oligonucleotides showing a level of mRNA % inhibition from > about 70% to about 100% include ISIS Nos. 12539 (phosphorothioate linkages), 15346 and 5 15347 ("gapmers"), and 15348 and 15351 (5' "wingmers") (SEQ ID NO: 16). Oligonucleotides showing levels of mRNA inhibition of from ≥ about 90% to about 100% of JNK1 mRNAs in this assay include ISIS Nos. 12539, 15345 AND 15346 (SEQ ID NO: 16). The oligonucleotides tested showed 10 approximately parallel levels of JNK1 protein inhibition; ISIS Nos. 12539, 15346-15348 and 15351 effected levels of protein inhibition ≥ about 40%, and ISIS Nos. 12539, 15346 and 15347 effected levels of protein inhibition ≥ about 55%.

15 At t=72 h, oligonucleotides showing a level of mRNA % inhibition from > about 70% to about 100% include ISIS Nos. 12539 (phosphorothioate linkages), 15346 and 15347 ("gapmers"), and 15348 (5' "wingmers") (SEQ ID NO: 16). Oligonucleotides showing levels of mRNA inhibition of from 20 ≥ about 90% to about 100% of JNK1 mRNAs at this point in the assay include ISIS Nos. 12539 and 15346 (SEQ ID NO: 16). Overall, the oligonucleotides tested showed higher levels of JNK1 protein inhibition at this point in the assay. With the exception of the fully 2'-methoxyethoxy- 25 modified ISIS 15345, all of the oligonucleotides in Table 7 effect ≥ about 40% protein inhibition. ISIS Nos. 12539, 15346-15348 and 15351 effected levels of protein inhibition ≥ about 60%, and ISIS Nos. 12539, 15346 and 15347 effected levels of protein inhibition ≥ about 70%.

- 78 -

TABLE 7  
**Modulation of JNK1 mRNA and JNK1 Protein Levels  
by Modified JNK1 Antisense Oligonucleotides**

ISIS #	SEQ ID NO:	RNA % Control	RNA % Inhibition	Protein % Control	Protein % Inhibition
<i>t = 48 h</i>					
control	---	100.0	0.0	100.0	0.0
12539	16	6.7	93.3	44.3	55.7
15345	16	70.3	29.7	105.0	(0.0)
15346	16	4.3	95.7	42.7	57.3
15347	16	7.9	92.1	38.8	61.2
15348	16	24.3	75.7	58.3	41.7
15349	16	63.1	36.9	69.5	30.5
15350	16	49.2	50.8	71.7	28.3
15351	16	26.9	73.1	52.4	47.6

- 79 -

ISIS #	SEQ ID NO:	% Control	RNA % Inhibition	RNA % Inhibition	Protein % Control	Protein % Inhibition
<b>t = 72 h</b>						
control	16	100.0	0.0	100.0	100.0	0.0
12539	16	11.7	88.3	29.2	70.8	
15345	16	187.4	(0.0)	87.8	12.2	
15346	16	10.6	89.4	25.7	74.3	
15347	16	8.2	81.8	28.4	71.6	
15348	16	28.0	72.0	41.7	58.3	
15349	16	52.0	48.0	56.5	43.5	
15350	16	54.4	45.6	58.4	41.6	
15351	16	46.1	53.9	37.0	63.0	

- 80 -

**G. Oligonucleotides specific for JNK1 isoforms:**

Subsequent to the initial descriptions of JNK1 (Derijard et al., *Cell*, 1994, 76, 1025), cDNAs encoding related isoforms of JNK1 were cloned and their nucleotide sequences 5 determined (Gupta et al., *EMBO Journal*, 1996, 15, 2760). In addition to JNK1- $\alpha$ 1 (GenBank accession No. L26318, locus name "HUMJNK1"), which encodes a polypeptide having an amino acid sequence identical to that of JNK1, the additional isoforms include JNK1- $\alpha$ 2 (GenBank accession No. 10 U34822, locus name "HSU34822"), JNK1- $\beta$ 1 (GenBank accession No. U35004, locus name "HSU35004") and JNK1- $\beta$ 2 (GenBank accession No. U35005, locus name "HSU35005"). The four isoforms of JNK1, which probably arise from alternative mRNA splicing, may each interact with different 15 transcription factors or sets of transcription factors (Gupta et al., *EMBO Journal*, 1996, 15, 2760). As detailed below, the oligonucleotides of the invention are specific for certain members or sets of these isoforms of JNK1.

In the ORFs of mRNAs encoding JNK1/JNK1- $\alpha$ 1 and JNK1- $\alpha$ 2, nucleotides (nt) 631-665 of JNK1/JNK1- $\alpha$ 1 (Genbank accession No. L26318) and nt 625-659 of JNK1- $\alpha$ 2 (Genbank accession No. U34822) have the sequence shown below as SEQ ID NO: 63, whereas, in the ORFs of mRNAs encoding JNK1- $\beta$ 1 and JNK1- $\beta$ 2, nt 631-665 of JNK1- $\beta$ 1 (GenBank accession No. 25 U35004) and nt 626-660 of JNK1- $\beta$ 2 (GenBank accession No. U35005) have the sequence shown below as SEQ ID NO: 64. For purposes of illustration, SEQ ID NOS: 63 and 64 are shown aligned with each other (vertical marks, "|," indicate bases that are identical in both sequences):

30 5'-AACGTGGATTATGGTCTGTGGGGTGCATTATGGG	SEQ ID NO: 63
5'-AACGTTGACATTTGGTCAGTTGGGTGCATCATGGG	SEQ ID NO: 64

- 81 -

Due to this divergence between the a and b JNK1 isoforms, antisense oligonucleotides derived from the reverse complement of SEQ ID NO: 63 (i.e., SEQ ID NO: 65, see below) can be used to modulate the expression of JNK1/JNK1-  
5  $\alpha$ 1 and JNK1- $\alpha$ 2 without significantly effecting the expression of JNK1- $\beta$ 1 and JNK1- $\beta$ 2. In like fashion, antisense oligonucleotides derived from the reverse complement of SEQ ID NO: 64 (i.e., SEQ ID NO: 66, see below) can be selected and used to modulate the expression  
10 of JNK1- $\beta$ 1 and JNK1- $\beta$ 2 without significantly effecting the expression of JNK1/JNK1- $\alpha$ 1 and JNK1- $\alpha$ 2. As an example, an oligonucleotide having a sequence derived from SEQ ID NO:  
15 65 but not to SEQ ID NO: 66 is specifically hybridizable to mRNAs encoding JNK1/JNK1- $\alpha$ 1 and JNK1- $\alpha$ 2 but not to those encoding JNK1- $\beta$ 1 and JNK1- $\beta$ 2:

5'-CCCATATAATGCACCCCCACAGACCATAAATCCACGTT                   SEQ ID NO: 65  
||||||| ||||||||| ||| ||||| || | ||| |||||  
5'-CCCATGATGCACCCAACTGACCAAAATGTCAACGTT                   SEQ ID NO: 66

As a further example, in the ORFs of mRNAs encoding  
20 JNK1/JNK1- $\alpha$ 1 and JNK1- $\alpha$ 2, nt 668-711 of JNK1/JNK1- $\alpha$ 1 (Genbank accession No. L26318) and nt 662-705 of JNK1- $\alpha$ 2 (Genbank accession No. U34822) have the sequence shown below as SEQ ID NO: 67, whereas, in the ORFs of mRNAs encoding JNK1- $\beta$ 1 and JNK1- $\beta$ 2, nt 668-711 of JNK1- $\beta$ 1  
25 (GenBank accession No. U35004) and nt 663-706 of JNK1- $\beta$ 2 (GenBank accession No. U35005) have the sequence shown below as SEQ ID NO: 68. For purposes of illustration, SEQ

- 82 -

ID NOS: 67 and 68 are shown aligned with each other as follows:

5' -AAATGGTTGCCACAAAATCCTCTTCCAGGAAGGGACTATATT SEQ ID NO:  
67

5    ||||| |                    | | ||| ||||| | || | |||||  
5'-AAATGATCAAAGGTGGTGTTCAGGTACAGATCATATT SEQ ID NO:  
68

Due to this divergence between the a and b JNK1 isoforms, antisense oligonucleotides derived from the reverse

10 complement of SEQ ID NO: 67 (i.e., SEQ ID NO: 69, see  
below) are specifically hybridizable to mRNAs encoding, and  
may be selected and used to modulate the expression of,  
JNK1/JNK1- $\alpha$ 1 and JNK1- $\alpha$ 2 without significantly effecting  
the expression of JNK1- $\beta$ 1 and JNK1- $\beta$ 2. In like fashion,  
15 antisense oligonucleotides derived from the reverse  
complement of SEQ ID NO: 68 (i.e., SEQ ID NO: 70, see  
below) are specifically hybridizable to mRNAs encoding, and  
may be selected and used to modulate the expression of, can  
be selected and used to modulate the expression of JNK1- $\beta$ 1  
20 and JNK1- $\beta$ 2 without significantly effecting the expression  
of JNK1/JNK1- $\alpha$ 1 and JNK1- $\alpha$ 2;

5'-AATATAGTCCCTCCTGGAAAGAGGATTGTGGCAAACCATTT SEQ ID NO:  
69

25 5'-AATATGATCTGTACCTGGGAACAAAACACCACCTTGATCATTT SEQ ID NO:  
70

In the case of the carboxyl terminal portion of the JNK1 isoforms, JNK1/JNK1- $\alpha$ 1 shares identity with JNK1- $\beta$ 1; similarly, JNK1- $\alpha$ 2 and JNK1- $\beta$ 2 have identical carboxy terminal portions. The substantial differences in the amino acid sequences of these isoforms (5 amino acids in JNK1/JNK1- $\alpha$ 1 and JNK1- $\beta$ 1 are replaced with 48 amino acids

in JNK1- $\alpha$ 2 and JNK1- $\beta$ 2) result from a slight difference in nucleotide sequence that shifts the reading frame. Specifically, in the ORFs of mRNAs encoding JNK1/JNK1- $\alpha$ 1 and JNK1- $\beta$ 1, nt 1144-1175 of JNK1/JNK1- $\alpha$ 1 (Genbank accession No. L26318) and JNK1- $\beta$ 1 (Genbank accession No. U35004) have the sequence shown below as SEQ ID NO: 71, whereas, in the ORFs of mRNAs encoding JNK1- $\alpha$ 2 and JNK1- $\beta$ 2, nt 1138-1164 of JNK1- $\alpha$ 2 (GenBank accession No. U34822) and nt 1139-1165 of JNK1- $\beta$ 2 (GenBank accession No. U35005) have the sequence shown below as SEQ ID NO: 72. For purposes of illustration, SEQ ID NOS: 71 and 72 are shown aligned with each other (dashes, “-,” indicate bases that are absent in the indicated sequence, and emboldened bases indicate the stop codon for the JNK1/JNK1- $\alpha$ 1 and JNK1- $\beta$ 1 ORFs):

15 5'-CCCTCTCCTTACAGCACAGGTGCAGCAGTGATC SEQ ID NO: 71  
          |||||||||          |||||||||  
5'-CCCTCTCCTTACAG----GTGCAGCAGTGATC SEQ ID NO: 72

Due to this divergence between the JNK1 isoforms, antisense oligonucleotides derived from the reverse complement of SEQ ID NO: 71 (i.e., SEQ ID NO: 73, see below) are specifically hybridizable to mRNAs encoding, and may be selected and used to modulate the expression of, JNK1/JNK1- $\alpha$ 1 and JNK1- $\beta$ 1 without significantly effecting the expression of JNK1- $\alpha$ 2 and JNK1- $\beta$ 2. In like fashion, antisense oligonucleotides derived from the reverse complement of SEQ ID NO: 72 (i.e., SEQ ID NO: 74, see below) are specifically hybridizable to mRNAs encoding, and may be selected and used to modulate the expression of, JNK1- $\alpha$ 2 and JNK1- $\beta$ 2 without significantly effecting the expression of JNK1/JNK1- $\alpha$ 1 and JNK1- $\beta$ 1:

- 84 -

5'-GATCACTGCTGCACCTGTGCTAAAGGAGAGGG                         5'-GATCACTGCTGCAC----CTAAAGGAGAGGG	SEQ ID NO: 73 SEQ ID NO: 74
--	--------------------------------

In preferred embodiments, such isoform-specific  
5 oligonucleotides such as are described above are  
methoxyethoxy "gapmers" or "wingmers" in which the RNase H-  
sensitive "gap" or "wing" is positioned so as to overlap a  
region of nonidentity in the above antisense sequences,  
*i.e.*, SEQ ID NOS: 65, 66, 69, 70, 73 and 74.

10 **Example 4: Oligonucleotide-Mediated Inhibition of JNK2  
Expression**

A. **JNK2 oligonucleotide sequences:** Table 8 lists the nucleotide sequences of oligonucleotides designed to specifically hybridize to JNK2 mRNAs and the corresponding 15 ISIS and SEQ ID numbers thereof. The target gene nucleotide co-ordinates and gene target region are also included. The nucleotide co-ordinates are derived from GenBank accession No. L31951, locus name "HUMJNK2" (see also Figure 1(A) of Sluss et al., *Mol. Cel. Biol.*, 1994, 20 14, 8376, and Kallunki et al., *Genes & Development*, 1994, 8, 2996). The abbreviations for gene target regions are as follows: 5'-UTR, 5' untranslated region; tIR, translation initiation region; ORF, open reading frame; 3'-UTR, 3' untranslated region. The nucleotides of the 25 oligonucleotides whose sequences are presented in Table 8 are connected by phosphorothioate linkages and are unmodified at the 2' position (*i.e.*, 2-deoxy). It should be noted that the oligonucleotide target co-ordinate positions and gene target regions may vary within mRNAs 30 encoding related isoforms of JNK2 (see subsection G, below).

In addition to hybridizing to human JNK2 mRNAs, the full oligonucleotide sequence of ISIS No. 12562 (SEQ ID NO: 33) hybridizes to the ORF of mRNAs from *Rattus norvegicus* that encode a stress-activated protein kinase named "p54 $\alpha$ 2" 5 (Kyriakis et al., *Nature*, 1994, 369, 156). Specifically, ISIS 12562 (SEQ ID NO: 33) hybridizes to bases 649-668 of GenBank accession No. L27112, locus name "RATSAPKB." This oligonucleotide is thus a preferred embodiment of the invention for investigating the role of the p54 $\alpha$ 2 protein 10 kinase in rat *in vitro*, i.e., in cultured cells or tissues derived from whole animals, or *in vivo*.

**B. JNK2-specific probes:** In initial screenings of a set of oligonucleotides derived from the JNK2 sequence (Table 9) for biological activity, a cDNA clone of JNK2 15 (Kallunki et al., *Genes & Development*, 1994, 8, 2996) was radiolabeled and used as a JNK2-specific probe in Northern blots. Alternatively, however, one or more of the oligonucleotides of Table 8 is detectably labeled and used as a JNK2-specific probe.

**C. Activities of JNK2 oligonucleotides:** The data 20 from screening a set of JNK2-specific phosphorothioate oligonucleotides (Table 9) indicate the following results. Oligonucleotides showing activity in this assay, as reflected by levels of inhibition from  $\geq$  about 50% to about 25 100% of JNK2 mRNA levels, include ISIS Nos. 12558, 12559, 12560, 12563, 12564, 12565, 12566, 12567, 12568, 12569 and 12570 (SEQ ID NOS: 29, 30, 31, 34, 35, 36, 37, 38, 39, 40 and 41, respectively). These oligonucleotides are thus preferred embodiments of the invention for modulating JNK2 30 expression. Oligonucleotides showing levels of inhibition of from  $\geq$  about 80% to about 100% of JNK2 mRNAs in this assay, include ISIS Nos. 12558, 12560, 12565, 12567, 12568 and 12569 (SEQ ID NOS: 29, 31, 36, 38, 39 and 40,

- 86 -

respectively). These oligonucleotides are thus more preferred embodiments of the invention for modulating JNK2 expression.

The time course of inhibition of JNK2 mRNA expression  
5 by ISIS 12560 (SEQ ID NO: 31) is shown in Table 10.

Following the 4 hour treatment with ISIS 12560, the level of inhibition of JNK2 was greater than or equal to about 80% for at least about 12 hours and greater than or equal to about 60% up to at least about t=48 h.

- 87 -

TABLE 8  
Nucleotide Sequences of JNK2 Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE (5' -> 3')	SEQ ID NO:	TARGET NUCLEOTIDE CO-ORDINATES	GENE TARGET REGION
12558	GTT-TCA-GAT-CCC-TCG-CCC-GC	29	0003-0022	5'-UTR
12559	TGC-AGC-ACA-AAC-AAT-CCC-TT	30	0168-0187	ORF
12560	GTC-CGG-GCC-AGG-CCA-AAG-TC	31	0563-0582	ORF
12561	CAG-GAT-GAC-TTC-GGG-CGC-CC	32	0633-0652	ORF
12562	GCT-CTC-CCA-TGA-TGC-AAC-CC	33	0691-0710	ORF
12563	ATG-GGT-GAC-GCA-GAG-CTT-CG	34	0997-1016	ORF
12564	CTG-CTG-CAT-CTG-AAG-GCT-GA	35	1180-1199	ORF
12565	TGA-GAA-GGA-GTG-GCG-TTG-CT	36	1205-1224	ORF
12566	TGC-TGT-CTG-TGT-CTG-AGG-CC	37	1273-1292	ORF
12567	GGT-CCC-GTC-GAG-GCA-TCA-AG	38	1295-1314	ORF

- 88 -

12568	CAT-TTC-AGG-CCC-ACG-GAG-GT	39	1376-1395	3' -UTR
12569	GGT-CTG-AAT-AGG-GCA-AGG-CA	40	1547-1566	3' -UTR
12570	GGG-CAA-GTC-CAA-GCA-AGC-AT	41	1669-1688	3' -UTR

- 89 -

TABLE 9

## Activities of JNK2 Oligonucleotides

	ISIS NO.	SEQ ID NO:	GENE TARGET REGION	% EXPRESSION	% INHIBITION
5	12558	29	5'-UTR	15%	85%
	12559	30	ORF	28%	72%
	12560	31	ORF	11%	89%
	12561	32	ORF	60%	40%
	12562	30	ORF	89%	11%
10	12563	34	ORF	22%	78%
	12564	35	ORF	28%	72%
	12565	36	ORF	19%	81%
	12566	37	ORF	42%	58%
	12567	38	ORF	18%	82%
15	12568	39	3'-UTR	20%	80%
	12566	40	3'-UTR	13%	87%
	12570	41	3'-UTR	24%	76%

- 90 -

**TABLE 10**  
**Time Course of Response to JNK2 Antisense**  
**Oligonucleotides (ASOs)**

ISIS #	SEQ ID NO:	ASO Description	Time	Normalized % Control	% Inhibition
<hr/>					
5	control	---	(LIPOFECTIN™ only)	0 h	100.0
	control	---	"	4 h	100.0
	control	---	"	12 h	100.0
	control	---	"	48 h	100.0
	control	---	"	72 h	100.0
<hr/>					
10	12560	31	JNK2 active	0 h	20.2
	12560	31	"	4 h	11.1
	12560	31	"	12 h	21.8
	12560	31	"	48 h	42.7
	12560	31	"	72 h	116.8 (0.0)

15           **D. Additional JNK2 oligonucleotides:** The results for JNK2-specific oligonucleotides (Table 9) indicate that one of the most active phosphorothioate oligonucleotides for modulating JNK2 expression is ISIS 12560 (SEQ ID NO: 31). As detailed in Table 11, additional oligonucleotides based 20 on this oligonucleotide were designed to confirm and extend the findings described above.

- 91 -

Oligonucleotides ISIS Nos. 14318 (SEQ ID NO: 42) and 14319 (SEQ ID NO: 43) are 2'-deoxy-phosphorothioate sense strand and scrambled controls for ISIS 12560 (SEQ ID NO: 31), respectively. ISIS Nos. 15353 and 15354 are "gapmers" corresponding to ISIS 12560; both have 2'-methoxyethoxy "wings" (having phosphorothioate linkages in the case of ISIS 15353 and phosphodiester linkages in the case of ISIS 15354) and a central 2'-deoxy "gap" designed to support RNaseH activity on the target mRNA molecule. Similarly, ISIS Nos. 15355 to 15358 are "wingmers" corresponding to ISIS 12560 and have a 5' or 3' 2'-methoxyethoxy RNaseH-refractory "wing" and a 3' or 5' (respectively) 2-deoxy "wing" designed to support RNaseH activity on the target JNK2 mRNA.

The chemically modified derivatives of ISIS 12560 (SEQ ID NO: 31) were tested in the Northern assay described herein at concentrations of 100 and 400 nM, and the data (Table 12) indicate the following results. At 400 nM, relative to the 2'-unmodified oligonucleotide ISIS 12560, both "gapmers" (ISIS Nos. 15353 and 15354) effected inhibition of JNK2 mRNA expression up to at least about 80% inhibition. Similarly, the four "wingmers" (ISIS Nos. 15355 to 15358) effected inhibition of JNK2 expression of up to at least about 70 to 90% inhibition.

**E. Dose- and sequence-dependent response to JNK2 oligonucleotides:** In order to demonstrate a dose-dependent response to ISIS 12560 (SEQ ID NO: 31), different concentrations (i.e., 50, 100, 200 and 400 nM) of ISIS 12560 were tested for their effect on JNK2 mRNA levels in A549 cells (Table 13). In addition, two control oligonucleotides (ISIS 14318, SEQ ID NO: 42, sense control, and ISIS 14319, SEQ ID NO: 43, scrambled control; see also Table 11) were also applied to A549 cells in order to

- 92 -

demonstrate the specificity of ISIS 12560. The results (Table 12) demonstrate that the response of A549 cells to ISIS 12539 is dependent on dose in an approximately linear fashion. In contrast, neither of the control 5 oligonucleotides effect any consistent response on JNK2 mRNA levels.

**TABLE 11**

**Chemically Modified JNK2 Oligonucleotides**

	<b>ISIS NO.</b>	<b>NUCLEOTIDE SEQUENCE (5' -&gt; 3') AND CHEMICAL MODIFICATIONS*</b>	<b>SEQ ID NO:</b>	<b>COMMENTS</b>
10	12560	G <sup>s</sup> T <sup>s</sup> C <sup>s</sup> C <sup>s</sup> G <sup>s</sup> G <sup>s</sup> G <sup>s</sup> C <sup>s</sup> C <sup>s</sup> A <sup>s</sup> G <sup>s</sup> G <sup>s</sup> C <sup>s</sup> C <sup>s</sup> A <sup>s</sup> A <sup>s</sup> A <sup>s</sup> G <sup>s</sup> T <sup>s</sup> C	31	active
	14318	G <sup>s</sup> A <sup>s</sup> C <sup>s</sup> T <sup>s</sup> T <sup>s</sup> T <sup>s</sup> G <sup>s</sup> G <sup>s</sup> C <sup>s</sup> C <sup>s</sup> T <sup>s</sup> G <sup>s</sup> G <sup>s</sup> C <sup>s</sup> C <sup>s</sup> C <sup>s</sup> G <sup>s</sup> G <sup>s</sup> A <sup>s</sup> C	42	12560 sense control
	14319	G <sup>s</sup> T <sup>s</sup> G <sup>s</sup> C <sup>s</sup> G <sup>s</sup> C <sup>s</sup> G <sup>s</sup> C <sup>s</sup> G <sup>s</sup> A <sup>s</sup> G <sup>s</sup> C <sup>s</sup> C <sup>s</sup> C <sup>s</sup> G <sup>s</sup> A <sup>s</sup> A <sup>s</sup> A <sup>s</sup> T <sup>s</sup> C	43	scrambled control
15	15352	G <sup>s</sup> T <sup>s</sup> C <sup>s</sup> C <sup>s</sup> G <sup>s</sup> G <sup>s</sup> G <sup>s</sup> C <sup>s</sup> C <sup>s</sup> A <sup>s</sup> G <sup>s</sup> G <sup>s</sup> C <sup>s</sup> C <sup>s</sup> S <sup>s</sup> A <sup>s</sup> A <sup>s</sup> A <sup>s</sup> G <sup>s</sup> T <sup>s</sup> C	31	fully 2'-methoxyeth oxy
	15353	G <sup>s</sup> T <sup>s</sup> C <sup>s</sup> C <sup>s</sup> G <sup>s</sup> G <sup>s</sup> G <sup>s</sup> C <sup>s</sup> C <sup>s</sup> A <sup>s</sup> G <sup>s</sup> G <sup>s</sup> C <sup>s</sup> C <sup>s</sup> S <sup>s</sup> A <sup>s</sup> A <sup>s</sup> A <sup>s</sup> G <sup>s</sup> T <sup>s</sup> C	31	"gapmer"
	15354	G <sup>o</sup> T <sup>o</sup> C <sup>o</sup> G <sup>s</sup> G <sup>s</sup> G <sup>s</sup> C <sup>s</sup> C <sup>s</sup> A <sup>s</sup> G <sup>s</sup> G <sup>s</sup> C <sup>s</sup> C <sup>s</sup> S <sup>s</sup> A <sup>o</sup> A <sup>o</sup> A <sup>o</sup> G <sup>o</sup> T <sup>o</sup> C	31	"gapmer"
	15355	G <sup>s</sup> T <sup>s</sup> C <sup>s</sup> C <sup>s</sup> G <sup>s</sup> G <sup>s</sup> G <sup>s</sup> C <sup>s</sup> C <sup>s</sup> A <sup>s</sup> G <sup>s</sup> G <sup>s</sup> C <sup>s</sup> C <sup>s</sup> S <sup>s</sup> A <sup>s</sup> A <sup>s</sup> A <sup>s</sup> G <sup>s</sup> T <sup>s</sup> C	31	"wingmer"
	15356	G <sup>s</sup> T <sup>s</sup> C <sup>s</sup> C <sup>s</sup> G <sup>s</sup> G <sup>s</sup> G <sup>s</sup> C <sup>s</sup> C <sup>s</sup> A <sup>s</sup> G <sup>s</sup> G <sup>s</sup> C <sup>s</sup> C <sup>s</sup> S <sup>s</sup> A <sup>s</sup> A <sup>s</sup> A <sup>s</sup> G <sup>s</sup> T <sup>s</sup> C	31	"wingmer"
	15358	G <sup>o</sup> T <sup>o</sup> C <sup>o</sup> G <sup>o</sup> G <sup>o</sup> C <sup>o</sup> C <sup>o</sup> A <sup>o</sup> G <sup>s</sup> G <sup>s</sup> C <sup>s</sup> C <sup>s</sup> S <sup>s</sup> A <sup>s</sup> A <sup>s</sup> A <sup>s</sup> G <sup>s</sup> T <sup>s</sup> C	31	"wingmer"

- 93 -

15357	G <sup>s</sup> T <sup>s</sup> C <sup>s</sup> C <sup>s</sup> G <sup>s</sup> G <sup>s</sup> G <sup>s</sup> C <sup>s</sup> C <sup>s</sup> <b>A<sup>0</sup>G<sup>0</sup>G<sup>0</sup>C<sup>0</sup>C<sup>0</sup>A<sup>0</sup>A<sup>0</sup>G<sup>0</sup>T<sup>0</sup>C</b>	31	"wingmer"
20572	G <sup>s</sup> T <sup>s</sup> C <sup>s</sup> C <sup>s</sup> G <sup>s</sup> G <sup>s</sup> <u>C<sup>s</sup>C<sup>s</sup>A<sup>s</sup>G<sup>s</sup>G<sup>s</sup><u>C<sup>s</sup>C<sup>s</sup>A<sup>s</sup>A<sup>s</sup>G<sup>s</sup>T<sup>s</sup>C</u></u>	31	fully 5-methyl-cytosine version of ISIS 15353

\*Emboldened residues, 2'-methoxyethoxy- residues (others are 2'-deoxy-) including "C" residues, 5-methyl-cytosines; "o", 5 phosphodiester linkage; "s", phosphorothioate linkage.  
 --- "C" residues, 2'-deoxy 5-methylcytosine residues; ---

**TABLE 12**  
**Activity of Chemically Modified JNK2 Antisense Oligonucleotides**

10	ISIS #	SEQ ID NO:	Oligonucleotide Description	Dose	Normalized % Control
	control	---	No oligonucleotide (LIPOFECTIN™ only)	---	100.0
15	12560	31	JNK2 active, fully P=S & fully 2'-deoxy	100 nM	62.1
	12560	31		400 nM	31.4
	15352	31	fully P=S & fully 2'-MOE	100 nM	132.4
	15352	31		400 nM	158.4
	15353	31	gapmer: P=S, 2'-MOE wings;	100 nM	56.7
	15353	31		400 nM	21.2
	15354	31	gapmer: P=O, 2'-MOE wings;	100 nM	38.3

- 94 -

15354	31	P=S, 2-deoxy core	400 nM	17.1
15355	31	wingmer: fully P=S;	100 nM	61.3
15355	31	5' 2'-MOE; 3' 2-deoxy	400 nM	29.1
15356	31	wingmer: fully P=S;	100 nM	38.6
5	15356	5' 2-deoxy; 3' 2'-MOE	400 nM	11.0
15358	31	wingmer: 5' P=O & 2'-MOE;	100 nM	47.4
15358	31	3' P=S & 2-deoxy	400 nM	29.4
15357	31	wingmer: 5' P=S & 2'-	100 nM	42.8
15357	31	deoxy; 3' P=O & 2'-MOE	400 nM	13.7

10

**TABLE 13****Dose-Dependent Responses to JNK2 Antisense Oligonucleotides**

ISIS #	SEQ ID NO:	Oligonucleotide Description	Dose	Normalized % Control
control	---	No oligonucleotide (LIPOFECTIN™ only)	---	100.0
12560	31	JNK2 active	50 nM	68.1
15	12560	"	100 nM	50.0
12560	31	"	200 nM	25.1
12560	31	"	400 nM	14.2
14318	42	12560 sense control	50 nM	87.1
20	14318	"	100 nM	89.8
14318	42	"	200 nM	92.1
14318	42	"	400 nM	99.6

- 95 -

14319	43	12560 scrambled control	50 nM	90.4
14319	43	"	100 nM	93.7
14319	43	"	200 nM	110.2
14319	43	"	400 nM	100.0

5       **F. Western Assays:** In order to assess the effect of oligonucleotides targeted to JNK2 mRNAs on JNK2 protein levels, Western assays are performed essentially as described above in Examples 2 and 3. A primary antibody that specifically binds to JNK2 is purchased from, for  
10 example, Santa Cruz Biotechnology, Inc., Santa Cruz, CA; Upstate Biotechnology, Inc., Lake Placid, NY; StressGen Biotechnologies, Inc., Victoria, BC, Canada; or Research Diagnostics, Inc., Flanders, NJ.

**G. Oligonucleotides specific for JNK2 isoforms:**

15 Subsequent to the initial descriptions of JNK2 (Sluss et al., *Mol. Cel. Biol.*, 1994, 14, 8376; Kallunki et al., *Genes & Development*, 1994, 8, 2996; GenBank accession No. HSU09759, locus name "U09759"), cDNAs encoding related isoforms of JNK2 were cloned and their nucleotide sequences  
20 determined (Gupta et al., *EMBO Journal*, 1996, 15, 2760). In addition to JNK2- $\alpha$ 2 (GenBank accession No. L31951, locus name "HUMJNK2"), which encodes a polypeptide having an amino acid sequence identical to that of JNK2, the additional isoforms include JNK2- $\alpha$ 1 (GenBank accession No.  
25 U34821, locus name "HSU34821"), JNK2- $\beta$ 1 (GenBank accession No. U35002, locus name "HSU35002") and JNK2- $\beta$ 2 (GenBank accession No. U35003, locus name "HSU35003"). The four isoforms of JNK2, which probably arise from alternative mRNA splicing, may each interact with different

transcription factors or sets of transcription factors (Gupta et al., *EMBO Journal*, 1996, 15, 2760). As detailed below, the oligonucleotides of the invention are specific for certain members or sets of these isoforms of JNK2.

5 In the ORFs of mRNAs encoding JNK2/JNK2- $\alpha$ 2 and JNK2-  
 $\alpha$ 1, nucleotides (nt) 689-748 of JNK2/JNK2- $\alpha$ 2 (GenBank  
accession No. L31951) and nt 675-734 of JNK2- $\alpha$ 1 (GenBank  
accession No. U34821) have the sequence shown below as SEQ  
ID NO: 75, whereas, in the ORFs of mRNAs encoding JNK2- $\beta$ 1  
10 and JNK2- $\beta$ 2, nt 653-712 of JNK2- $\beta$ 1 (GenBank accession No.  
U35002) and nt 665-724 of JNK2- $\beta$ 2 (GenBank accession No.  
U35003) have the sequence shown below as SEQ ID NO: 76.  
For purposes of illustration, SEQ ID NOS: 75 and 76 are  
shown aligned with each other (vertical marks, "|,"  
15 indicate bases that are identical in both sequences):

SEQ ID NO: 75

5'-GTGGGTTGCATCATGGGAGAGCTGGTGAAGGTTGTGTGATATTCCAAGGCACTGACCAT  
|||.....|||.....|||.....|||.....|||.....|||.....|||.....|||.....|||.....|||  
5'-GTCGGGTGCATCATGGCAGAAAATGGTCCTCCATAAAAGTCTGTCCC GGGAAGAGACTAT

20 Due to this divergence between the a and b JNK2 isoforms,  
antisense oligonucleotides derived from the reverse  
complement of SEQ ID NO: 75 (i.e., SEQ ID NO: 77, see  
below) are specifically hybridizable to, and may be  
25 selected and used to modulate the expression of, JNK2/JNK2-  
 $\alpha$ 2 and JNK2- $\alpha$ 1 without significantly effecting the  
expression of JNK1- $\beta$ 1 and JNK1- $\beta$ 2. In like fashion,  
antisense oligonucleotides derived from the reverse  
complement of SEQ ID NO: 76 (i.e., SEQ ID NO: 78, see  
30 below) are specifically hybridizable to, and may be  
selected and used to modulate the expression of, JNK2- $\beta$ 1  
and JNK2- $\beta$ 2 without significantly effecting the expression  
of JNK2/JNK2- $\alpha$ 2 and JNK2- $\alpha$ 1. As an example, an  
oligonucleotide having a sequence derived from SEQ ID NO:

- 97 -

77 but not from SEQ ID NO: 78 is specifically hybridizable  
to, mRNAs encoding JNK1/JNK1- $\alpha$ 1 and JNK1- $\alpha$ 2 but not to  
those encoding JNK2- $\beta$ 1 and JNK2- $\beta$ 2:

SEQ ID NO: 77

5' -ATGGTCAGTGCCTTGGAAATATCACACAACCTTCACCACTCTCCATGATGCAACCCAC  
           |||||    |||||    |||||    |||    |||||    |||||  
 5' -ATAGTCTCTTCCCAGGGAACAGGACTTATGGAGGACCATTTCTGCCATGATGCACCCGAC

SEQ ID NO: 78

In the case of the carboxyl terminal portion of the JNK2 isoforms, JNK2/JNK2- $\alpha$ 2 shares identity with JNK1- $\beta$ 2; similarly, JNK2- $\alpha$ 1 and JNK2- $\beta$ 1 have identical carboxy terminal portions. The substantial differences in the amino acid sequences of these isoforms (5 amino acids in JNK2- $\alpha$ 2 and JNK2- $\beta$ 2 are replaced with 47 amino acids in JNK2/JNK2- $\alpha$ 2 and JNK2- $\beta$ 2) result from a slight difference in nucleotide sequence that shifts the reading frame. Specifically, in the ORFs of mRNAs encoding JNK2- $\alpha$ 1 and JNK1- $\beta$ 1, nt 1164-1198 of JNK2- $\alpha$ 1 (GenBank accession No. U34821) and nt 1142-1176 of JNK2- $\beta$ 1 (GenBank accession No. U35002) have the sequence shown below as SEQ ID NO: 79, whereas, in the ORFs of mRNAs encoding JNK2/JNK2- $\alpha$ 2 and JNK2- $\beta$ 2, nt 1178-1207 of JNK2/JNK2- $\alpha$ 2 (GenBank accession No. L31951) and nt 1154-1183 of JNK2- $\beta$ 2 (GenBank accession No. U35003) have the sequence shown below as SEQ ID NO: 80. For purposes of illustration, SEQ ID NOS: 79 and 80 are shown aligned with each other (dashes, "-", indicate bases that are absent in the indicated sequence, and emboldened bases indicate the stop codon for the JNK2- $\alpha$ 1 and JNK2- $\beta$ 1 ORFs):

Due to this divergence between the JNK2 isoforms, antisense oligonucleotides derived from the reverse complement of SEO

- 98 -

In preferred embodiments, such isoform-specific oligonucleotides such as are described above are methoxyethoxy "gapmers" or "wingmers" in which the RNase H-sensitive "gap" or "wing" is positioned so as to overlap a 25 region of nonidentity in the above antisense sequences, i.e., SEQ ID NOS: 77, 78, 81 and 82.

## **Example 5: Oligonucleotide-Mediated Inhibition of JNK3**

### **Expression**

**A. JNK3 oligonucleotide sequences:** Table 14 lists the nucleotide sequences of oligonucleotides designed to specifically hybridize to JNK3 mRNAs and the corresponding ISIS and SEQ ID numbers thereof. The target gene

- 99 -

nucleotide co-ordinates and gene target region are also included. The nucleotide co-ordinates are derived from GenBank accession No. U07620, locus name "HSU07620" see also Figure 4(A) of Mohit et al., *Neuron*, 1994, 14, 67).

- 5 The abbreviations for gene target regions are as follows:  
5'-UTR, 5' untranslated region; tIR, translation initiation  
region; ORF, open reading frame; 3'-UTR, 3' untranslated  
region. It should be noted that the oligonucleotide target  
co-ordinate positions and gene target regions may vary  
10 within mRNAs encoding related isoforms of JNK3 (see  
subsection D, below).

The nucleotides of the oligonucleotides whose sequences are presented in Table 14 are connected by phosphorothioate linkages and are "gapmers." Specifically,  
15 the six nucleotides of the 3' and 5' termini are 2'-  
methoxyethoxy- modified and are shown emboldened in Table  
14, whereas the central eight nucleotides are unmodified at  
the 2' position (i.e., 2-deoxy).

In addition to hybridizing to human JNK3 mRNAs, the  
20 full oligonucleotide sequences of ISIS Nos. 16692, 16693,  
16703, 16704, 16705, 16707, and 16708 (SEQ ID NOS: 46, 47,  
56, 57, 58, 60 and 61, respectively) specifically hybridize  
to mRNAs from *Rattus norvegicus* that encode a stress-  
activated protein kinase named "p54 $\beta$ " (Kyriakis et al.,  
25 *Nature*, 1994, 369, 156; GenBank accession No. L27128, locus  
name "RATSAPKC." Furthermore, the full oligonucleotide  
sequences of 16692, 16693, 16695, 16703, 16704, 16705,  
16707 and 16708 (SEQ ID NOS: 46, 47, 49, 56, 57, 58, 60 and  
61, respectively) specifically hybridize to mRNAs from *Mus*  
30 *musculus* that encode a mitogen activated protein (MAP)  
kinase stress activated protein named the "p459<sup>3F12</sup> SAP  
kinase" (Martin et al., *Brain Res. Mol. Brain Res.*, 1996,  
35, 47; GenBank accession No. L35236, locus name

- 100 -

"MUSMAPK"). These oligonucleotides are thus preferred embodiments of the invention for investigating the role of the p54 $\beta$  and p45 $^{9F12}$  SAP protein kinases in rat or mouse, respectively, *in vitro*, i.e., in cultured cells or tissues 5 derived from whole animals or *in vivo*. The target gene nucleotide co-ordinates and gene target regions for these oligonucleotides, as defined for these GenBank entries, are detailed in Table 15.

**B. JNK3-specific probes:** In initial screenings of a 10 set of oligonucleotides derived from the JNK3 sequence for biological activity, a cDNA clone of JNK3 (Derijard et al., Cell, 1994, 76, 1025) was radiolabeled and used as a JNK3-specific probe in Northern blots. Alternatively, however, one or more of the oligonucleotides of Table 14 is 15 detectably labeled and used as a JNK3-specific probe.

**C. Western Assays:** In order to assess the effect of 20 oligonucleotides targeted to JNK3 mRNAs on JNK3 protein levels, Western assays are performed essentially as described above in Examples 2 through 4. A primary antibody that specifically binds to JNK3 is purchased from, for example, Upstate Biotechnology, Inc. (Lake Placid, NY), StressGen Biotechnologies Corp. (Victoria, BC, Canada), or New England Biolabs, Inc. (Beverly, MA).

TABLE 14  
Nucleotide Sequences of JNK3 Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE <sup>1</sup> (5' -> 3')	SEQ ID NO:	TARGET GENE NUCLEOTIDE CO-ORDINATES	GENE TARGET REGION
5 16690	TTC-AAC-AGT-TTC-TTG-CAT-AA	44	0157-0176	5'-UTR
16691	CTC-ATC-TAT-AGG-AAA-CGG-GT	45	0182-0200	5'-UTR
16692	TGG-AGG-CTC-ATA-AAT-ACC-AC	46	0215-0234	tIR
16693	TAT-AAG-AAA-TGG-AGG-CTC-AT	47	0224-0243	tIR
16694	TCA-CAT-CCA-ATG-TTG-GTT-CA	48	0253-0272	ORF
16695	TTA-TCG-AAT-CCC-TGA-CAA-AA	49	0281-0300	ORF
16696	GTT-TGG-CAA-TAT-ATG-ACA-CA	50	0310-0329	ORF
16697	CTG-TCA-AGG-ACA-GCA-TCA-TA	51	0467-0486	ORF
16698	AAT-CAC-TTG-ACA-TAA-GTT-GG	52	0675-0694	ORF
16699	TAA-ATC-CCT-GTG-AAT-TAT-TC	53	0774-0793	ORF
15 16700	GCA-TCC-CAC-AGA-CCA-TAT-AT	54	0957-0976	ORF

ISIS NO.	NUCLEOTIDE SEQUENCE <sup>1</sup> (5' -> 3')	SEQ ID NO:	TARGET NUCLEOTIDE CO-ORDINATES	GENE TARGET REGION
16702	<b>TGT-TCT-CTT-TCA-TCC-AAC-TG</b>	55	1358-1377	ORF
16703	<b>TCT-CAC-TGC-TGT-TCA-CTG-CT</b>	56	1485-1504	tIR
16704	<b>GGG-TCT-GGT-CGG-TGG-ACA-TG</b>	57	1542-1561	3'-UTR
16705	<b>AGG-CTG-CTG-TCA-GTG-TCA-GA</b>	5.8	1567-1586	3'-UTR
16706	<b>TCA-CCT-GCA-ACA-ACC-CAG-GG</b>	59	1604-1623	3'-UTR
16707	<b>GCG-GCT-AGT-CAC-CTG-CAA-CA</b>	60	1612-1631	3'-UTR
16708	<b>CGC-TGG-GTT-TCG-CAG-GCA-GG</b>	61	1631-1650	3'-UTR
16709	<b>ATC-ATC-TCC-TGA-AGA-ACG-CT</b>	62	1647-1666	3'-UTR

<sup>1</sup>Emboldened residues are 2'-methoxyethoxy- modified.

- 103 -

TABLE 15  
Rat and Mouse Gene Target Locations of JNK3 Oligonucleotides

	ISIS NO.	SEQ ID NO:	Rat p54 $\beta$ NUCLEOTIDE CO-ORDINATES <sup>1</sup>	GENE TARGET REGION	Mouse P459 $\beta$ F12 NUCLEOTIDE CO-ORDINATES <sup>2</sup>	GENE TARGET REGION
5	16692	46	0213-0232	5'-UTR	0301-0320	tIR
	16693	47	0222-0241	5'-UTR	0310-0329	tIR
	16695	49	---	---	0367-0386	ORF
	16703	56	1506-1525	ORF	1571-1590	tTR
	16704	57	1563-1582	ORF	1628-1647	3'-UTR
10	16705	58	1588-1607	ORF	1653-1672	3'-UTR
	16707	60	1633-1652	tTR	1698-1717	3'-UTR
	16708	61	1652-1671	3'-UTR	1717-1736	3'-UTR

<sup>1</sup>Co-ordinates from GenBank Accession No. L27128, locus name "RATSAPKC."

<sup>2</sup>Co-ordinates from GenBank Accession No. L35236, locus name "MUSMAPK."

- 104 -

D. Oligonucleotides specific for JNK3 isoforms: Two isoforms of JNK3 have been described. JNK3- $\alpha$ 1 was initially cloned and named "p49<sup>3F12</sup> kinase" by Mohit et al. (*Neuron*, 1995, 14, 67). Subsequently, two cDNAs encoding related isoforms of JNK3 were cloned and their nucleotide sequences determined (Gupta et al., *EMBO Journal*, 1996, 15, 2760). The isoforms are named JNK3- $\alpha$ 1 (GenBank accession No. U34820, locus name "HSU34820") and JNK3- $\alpha$ 2 (GenBank accession No. U34819, locus name "HSU34819") herein. The two isoforms of JNK3, which probably arise from alternative mRNA splicing, may each interact with different transcription factors or sets of transcription factors (Gupta et al., *EMBO Journal*, 1996, 15, 2760). As detailed below, certain oligonucleotides of the invention are specific for each of these isoforms of JNK3.

JNK3- $\alpha$ 1 and JNK- $\alpha$ 2 differ at their carboxyl terminal portions. The substantial differences in the amino acid sequences of these isoforms (5 amino acids in JNK3- $\alpha$ 1 are replaced with 47 amino acids in JNK3- $\alpha$ 2) result from a slight difference in nucleotide sequence that shifts the reading frame. Specifically, in the ORF of mRNAs encoding JNK3- $\alpha$ 1, nucleotides (nt) 1325-1362 of JNK3- $\alpha$ 1 (GenBank accession No. U34820) have the sequence shown below as SEQ ID NO: 83, whereas, in the ORF of mRNAs encoding JNK3- $\alpha$ 2, nt 1301-1333 of JNK3- $\alpha$ 2 (GenBank accession No. U34819) have the sequence shown below as SEQ ID NO: 84. For purposes of illustration, SEQ ID NOS: 83 and 202 are shown aligned with each other (vertical marks, "|," indicate bases that are identical in both sequences; dashes, "-", indicate bases that are absent in the indicated sequence; and emboldened bases indicate the stop codon for the JNK3- $\alpha$ 1 ORF):

- 105 -

5'-GGACAGCCTCTCCTTCAGCACAGGTGCAGCAGTGAAC       SEQ ID NO: 83  
||||| ||||| ||||| |||||           ||||| ||||| |||||  
5'-GGACAGCCTCTCCTTCAG-----GTGCAGCAGTGAAC       SEQ ID NO: 84

Due to this divergence between the JNK3 isoforms, antisense  
5 oligonucleotides derived from the reverse complement of SEQ  
ID NO: 83 (i.e., SEQ ID NO: 85, see below) are specifically  
hybridizable to mRNAs encoding, and may be selected and  
used to modulate the expression of JNK3- $\alpha$ 1 without  
significantly effecting the expression of JNK3- $\alpha$ 2. In like  
10 fashion, antisense oligonucleotides derived from the  
reverse complement of SEQ ID NO: 84 (i.e., SEQ ID NO: 86,  
see below) are specifically hybridizable to mRNAs encoding,  
and may be selected and used to modulate the expression of  
JNK3- $\alpha$ 2 without significantly effecting the expression of  
15 JNK3- $\alpha$ 1:

5'-GTTCACTGCTGCACCTGTGCTGAAGGAGAAGGCTGTCC       SEQ ID NO: 85  
||||| ||||| |||||           ||||| ||||| |||||  
5'-GTTCACTGCTGCAC-----CTGAAGGAGAAGGCTGTCC       SEQ ID NO: 86

In preferred embodiments, such isoform-specific  
20 oligonucleotides such as are described above are  
methoxyethoxy "gapmers" or "wingmers" in which the RNase H-  
sensitive "gap" or "wing" is positioned so as to overlap a  
region of nonidentity in the above antisense sequences,  
i.e., SEQ ID NOS: 85 and 86.

25       **E. Activities of JNK3 oligonucleotides:** The JNK3-  
specific phosphorothioate, 2'-methoxyethoxy "gapmer"  
oligonucleotides (Table 14) were screened for their ability  
to affect JNK3 mRNA levels in SH-SY5Y cells (Biedler et  
al., Cancer Res., 1973, 33, 2643). SH-SY5Y cells express a  
30 variety of mitogen-activated protein kinases (MAPKs; see,

- 106 -

e.g., Cheng et al., *J. Biol. Chem.*, 1998, 273, 14560). Cells were grown in DMEM essentially as previously described (e.g., Singleton et al., *J. Biol. Chem.*, 1996, 271, 31791; Jalava et al., *Cancer Res.*, 1990, 50, 3422) and 5 treated with oligonucleotides at a concentration of 200 nM as described in Example 2. Control cultures were treated with an aliquot of LIPOFECTIN™ that contained no oligonucleotide.

The results are shown in Table 16. Oligonucleotides 10 showing levels of inhibition from  $\geq$  about 45% to about 100% of JNK3 mRNA levels, include ISIS Nos. 16692, 16693, 16694, 16695, 16696, 16697, 16702, 16703, 16704, 16705 and 16706 (SEQ ID NOS:46, 47, 48, 49, 50, 51, 55, 56, 57, 58 and 59, respectively). These oligonucleotides are preferred 15 embodiments of the invention for modulating JNK3 expression. Oligonucleotides showing levels of inhibition of from  $\geq$  about 60% to about 100% of JNK3 mRNAs in this assay, wherein "about" indicates  $\pm 5\%$ , include ISIS Nos. 16693, 16694, 16695, 16702, 16703, 16704 and 16705 (SEQ ID 20 NOS:47, 48, 49, 55, 56, 57 and 58, respectively). These oligonucleotides are thus more preferred embodiments of the invention for modulating JNK3 expression.

**TABLE 16: Activities of JNK3 Oligonucleotides**

ISIS No:	SEQ ID NO:	GENE TARGET REGION	% EXPRESSION:	% INHIBITION:
control <sup>1</sup>	---	---	100%	0%
16690	44	5'-UTR	60%	40%
16691	45	5'-UTR	66%	34%
16692	46	tIR	47%	53%
16693	47	tIR	40%	60%

- 107 -

	<b>ISIS No:</b>	<b>SEQ ID NO:</b>	<b>GENE TARGET REGION</b>	<b>% EXPRESSION:</b>	<b>% INHIBITION:</b>
25	16694	48	ORF	42%	58%
	16695	49	ORF	44%	56%
	16696	50	ORF	55%	45%
	16697	51	ORF	54%	46%
5	16698	52	ORF	63%	37%
	16699	53	ORF	61%	39%
	16700	54	ORF	N.D. <sup>2</sup>	N.D.
	16702	55	ORF	39%	61%
10	16703	56	tTR	30%	70%
	16704	57	3'-UTR	36%	64%
	16705	58	3'-UTR	42%	58%
	16706	59	3'-UTR	45%	55%
15	16707	60	3'-UTR	73%	27%
	16708	61	3'-UTR	68%	32%
	16709	62	3'-UTR	66%	34%

<sup>1</sup> Cells treated with LIPOFECTIN™ only (no oligonucleotide).

<sup>2</sup> N.D., not determined.

**Example 6: Effect of Oligonucleotides Targeted to AP-1  
Subunits on Enzymes Involved in Metastasis**

20 Patients having benign tumors, and primary malignant tumors that have been detected early in the course of their development, may often be successfully treated by the surgical removal of the benign or primary tumor. If unchecked, however, cells from malignant tumors are spread throughout a patient's body through the processes of invasion and metastasis. Invasion refers to the ability of cancer cells to detach from a primary site of attachment

- 108 -

and penetrate, e.g., an underlying basement membrane. Metastasis indicates a sequence of events wherein (1) a cancer cell detaches from its extracellular matrices, (2) the detached cancer cell migrates to another portion of the 5 patient's body, often via the circulatory system, and (3) attaches to a distal and inappropriate extracellular matrix, thereby created a focus from which a secondary tumor can arise. Normal cells do not possess the ability to invade or metastasize and/or undergo apoptosis 10 (programmed cell death) if such events occur (Ruoslahti, *Sci. Amer.*, 1996, 275, 72).

The matrix metalloproteinases (MMPs) are a family of enzymes which have the ability to degrade components of the extracellular matrix (Birkedal-Hansen, *Current Op. Biol.*, 15 1995, 7, 728). Many members of the MMP family have been found to have elevated levels of activity in human tumors as well as other disease states (Stetler-Stevenson et al., *Annu. Rev. Cell Biol.*, 1993, 9, 541; Bernhard et al., *Proc. Natl. Acad. Sci. (U.S.A.)*, 1994, 91, 4293). In particular, 20 one member of this family, matrix metalloproteinase-9 (MMP-9), is often found to be expressed only in tumors and other diseased tissues (Himelstein et al., *Invasion & Metastasis*, 1994, 14, 246). Several studies have shown that regulation of the MMP-9 gene may be controlled by the AP-1 25 transcription factor (Kerr et al., *Science*, 1988, 242, 1242; Kerr et al., *Cell*, 1990, 61, 267; Gum et al., *J. Biol. Chem.*, 1996, 271, 10672; Hua et al., *Cancer Res.*, 1996, 56, 5279). In order to determine whether MMP-9 expression can be influenced by AP-1 modulation, the 30 following experiments were conducted on normal human epidermal keratinocytes (NHEKs). Although NHEKs normally express no detectable MMP-9, MMP-9 can be induced by a number of stimuli, including TPA (12-O-tetradecanoylphorbol

- 109 -

13-acetate). ISIS 10582, an oligonucleotide targeted to c-jun, was evaluated for its ability to modulate MMP-9 expression (see pending application Serial No. 08/837,201, filed April 14, 1997, attorney docket No. ISPH-0209. The 5 results (Table 16) demonstrate that ISIS 10582 is able to completely inhibit the expression of MMP-9 after induction with TPA.

TABLE 17

Effect of c-jun Oligonucleotide  
10 on MMP-9 Expression

Treatment	MMP-9
Basal	4
TPA - no oligo	100
10582: c-jun active	6
15 11562: sense control	99
11563: scrambled control	95
11564: mismatch control	89

These results demonstrate that c-Jun is required for TPA-mediated induction of MMP-9, and indicate that 20 oligonucleotides targeted to AP-1 subunits can inhibit the expression of MMP family members, thereby modulating the ability of cancer cells to invade other tissues and/or metastasize to other sites in a patient's body. Because JNK proteins activate AP-1 by phosphorylating the N-terminal portion of the Jun subunit thereof, modulation of one or more JNK proteins by the oligonucleotides of the present disclosure will also modulate the expression of MMP 25

- 110 -

family members and limit the metastatic ability of cancer cells.

**Example 7: Treatment of Human Tumors in Mice with Oligonucleotides Targeted to JNK Proteins**

5         Approximately  $5 \times 10^6$  breast adenocarcinoma cells (cell line MDA-MB-231; American Type Culture Collection, Richmond, VA, No. ATCC HTB-26) were implanted subcutaneously in the right inner thigh of nude mice (n=6 for each of three sets of mice). Oligonucleotides ISIS  
10 15346 (JNK1, SEQ ID NO:16) and 15353 (JNK2, SEQ ID NO:31) were suspended in saline and administered once daily to two sets of mice on the first day the tumor volume was about 100 mm<sup>3</sup>. A saline-only (0.9% NaCl) solution was given to a third set of animals as a control. Oligonucleotides were  
15 given by intravenous injection at a dosage of 25 mg/kg. Tumor size was measured and tumor volume was calculated on days 12, 19, 26 and 33 following tumor cell inoculation.

The results are shown in Table 18. Both 15346 (JNK1, SEQ ID NO:16) and 15353 (JNK2, SEQ ID NO:31) inhibited  
20 tumor growth compared to the saline control. Specifically, on days 26 and 33, the MDA-MB-231 tumors in animals that had been treated with the oligonucleotides had smaller volumes than the tumors in saline-treated animals, indicating that the oligonucleotides inhibited the growth  
25 of the tumors.

The antisense compounds of the invention are also tested for their ability to slow or eliminate the growth of xenografts resulting from, for example, human cervical epithelial carcinoma cells (HeLa cell line, ATCC No. ATCC  
30 CCL-2), human lung carcinoma cells (cell line A549, ATCC No. ATCC CCL-185), human adenocarcinoma cells (cell line SW480, ATCC No. ATCC CCL-228), human bladder carcinoma cells (cell line T24, ATCC No. HTB-4), human pancreatic

- 111 -

carcinoma cells (cell line MIA PaCa, ATCC No. CRL-1420) and human small cell carcinoma cells (cell line NCI-H69, ATCC HTB-119). Xenografts resulting from these and other cell lines are established using essentially the same techniques 5 as were used for the experiments using MDA-MB 231 cells.

**TABLE 18: Response of MDA-MB-231 Tumors in Mice to Oligonucleotides Targeted to JNK1 and JNK2**

Treatment:	Mean Tumor Volume (cm <sup>3</sup> )	Standard Deviation	Standard Error
Time			
<b>10 Saline:</b>			
Day 12	0.122	0.053	0.022
Day 19	0.253	0.078	0.032
Day 26	0.648	0.265	0.108
Day 33	1.560	0.887	0.362
<b>15 ISIS 15346 (JNK1):</b>			
Day 12	0.122	0.033	0.014
Day 19	0.255	0.099	0.040
Day 26	0.400	0.202	0.083
Day 33	0.638	0.416	0.170
<b>20 ISIS 15353 (JNK2):</b>			
Day 12	0.122	0.041	0.017
Day 19	0.230	0.072	0.029
Day 26	0.358	0.131	0.053
Day 33	0.762	0.366	0.150

**25 Example 8: Oligonucleotides Targeted to Genes Encoding Rat JNK Proteins**

In order to study the role of JNK proteins in animal models, oligonucleotides targeted to the genes encoding

- 112 -

JNK1, JNK2 and JNK3 of *Rattus norvegicus* were prepared. These oligonucleotides are 2'-methoxyethoxy, phosphodiester / 2'-hydroxyl, phosphorothioate / 2'-methoxyethoxy, phosphodiester "gapmers" in which every cytosine residue is 5-methylcytosine (m5c). These antisense compounds were synthesized according to the methods of the disclosure. Certain of these oligonucleotides are additionally specifically hybridizable to JNK genes from other species as indicated herein. The oligonucleotides described in 10 this Example were tested for their ability to modulate rat JNK mRNA levels essentially according to the methods described in the preceding Examples, with the exceptions that the cell line used was rat A10 aortic smooth muscle cells (ATCC No. ATCC CRL-1476) and the probes used were 15 specific for rat JNK1, JNK2 or JNK3 (see *infra*). A10 cells were grown and treated with oligonucleotides essentially as described by Cioffi et al. (*Mol. Pharmacol.*, 1997, 51, 383).

A. **JNK1:** Table 19 describes the sequences and 20 structures of a set of oligonucleotides, ISIS Nos. 21857 to 21870 (SEQ ID NOS:111 to 124, respectively) that were designed to be specifically hybridizable to nucleic acids from *Rattus norvegicus* that encode a stress-activated protein kinase named "p54 $\gamma$ " or "SAPK $\gamma$ " that is homologous 25 to the human protein JNK1 (Kyriakis et al., *Nature*, 1994, 369, 156; GenBank accession No. L27129, locus name "RATSAPKD"). In Table 19, emboldened residues are 2'-methoxyethoxy-residues (others are 2'-deoxy-); "C" residues are 2'-methoxyethoxy-5-methyl-cytosines and "C" residues 30 are 5-methyl-cytosines; "o" indicates a phosphodiester linkage; and "s" indicates a phosphorothioate linkage. The target gene co-ordinates are from GenBank Accession No. L27129, locus name "RATSAPKD."

TABLE 19:  
Nucleotide Sequences of Rat JNK1 Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE (5' -> 3')	SEQ ID NO	TARGET NUCLEOTIDE COORD	GENE TARGET REGION
21857	CoA o A o C o G s T s C s C s G s C s G s C s T s C s G o G o C o G	111	0002-0021	5'-UTR
21858	C o C o T o G o C s T s C s G s C s T s C s G s C s G o C o G o T o T	112	0029-0048	5'-UTR
21859	C o T o C o A o T s G s A s T s G s C s A s A s G s C s A o A o T o T o A	113	0161-0180	tIR
21860	T o G o T o G s T s C s A s C s G s T s T s T s A s C s T o T o C o T o G	114	0181-0200	ORF
21861	C o G o G o T o A s G s C s T s C s G s C s T s T s A s G o C o A o T o G	115	0371-0390	ORF
21862	C o T o A o G o G s A s T s T s T s G s G s T s G s G o T o G o T o G	116	0451-0470	ORF
21863	C o A o G o C o A s G s A s G s T s G s A s A s G s G s T s G o C o T o T o G	117	0592-0611	ORF
21864	T o C o G o T o T s C s C s T s G s C s A s G s T s C s C s T o T o G o C o C	118	0691-0710	ORF
21865	C o C o A o T o T s C s T s C s C s A s T s A s A s T o G o C o A o C	119	0811-0830	ORF
21866	T o G o A o A o T s T s C s A s G s G s A s C s A s A s G s G o T o G o T o T	120	0901-0920	ORF

ISIS NO.	NUCLEOTIDE SEQUENCE (5' -> 3')	SEQ ID NO	TARGET GENE NUCLEOTIDE COORD	GENE TARGET REGION
21867	AoGooCotoTsCsGstScTsAsCsGsGsAsGooAtoCoC	121	1101-1120	ORF
21868	CoAoCotoCsCstScTsAsTstScGstGstGocoToC	122	1211-1230	ORF
21869	GocoToGoCsAsCsCstScTsAsAsGSGsAsGooAcoGog	123	1301-1320	ORF
21870	CocoAoGooAsGstScGsGsAsTscstScTsGstGogoAoc	124	1381-1400	ORF

- 115 -

These antisense compounds were tested for their ability to modulate levels of p54γ (JNK1) and p54α (JNK2) mRNA in A10 cells via Northern assays. Due to the high degree of sequence identity between the human and rat genes, radiolabeled human JNK1 (Example 3) and JNK2 (Example 4) cDNAs functioned as specific probes for the rat homologs.

The results are shown in Table 20.  
Oligonucleotides showing levels of inhibition from ≥ about 10 75% to about 100% of rat JNK1 mRNA levels include ISIS Nos. 21857 to 21870 (SEQ ID NOS:111 to 124, respectively). These oligonucleotides are preferred embodiments of the invention for modulating rat JNK1 expression.  
Oligonucleotides showing levels of inhibition of from ≥ 15 about 90% to about 100% of rat JNK1 mRNAs in this assay include ISIS Nos. 21858, 21859, 21860, 21861, 21862, 21865, 21866 and 21867 (SEQ ID NOS:112, 113, 114, 115, 116, 119, 120 and 121, respectively). These oligonucleotides are thus more preferred embodiments of the invention for 20 modulating rat JNK1 expression. ISIS 21859 (SEQ ID NO:113) was chosen for use in further studies (*infra*).

Two of the oligonucleotides, ISIS Nos. 21861 and 21867 (SEQ ID NOS:115 and 121, respectively) demonstrated a capacity to modulate both JNK1 and JNK2. Such 25 oligonucleotides are referred to herein as "Pan JNK" antisense compounds because the term "Pan" is used in immunological literature to refer to an antibody that recognizes, e.g., all isoforms of a protein or subtypes of a cell type. The Pan JNK oligonucleotides are discussed in 30 more detail *infra*.

In addition to being specifically hybridizable to nucleic acids encoding rat JNK1, some of the oligonucleotides described in Table R-1 are also

- 116 -

specifically hybridizable with JNK1-encoding nucleic acids from other species. ISIS 21859 (SEQ ID NO:113) is complementary to bases 4 to 23 of cDNAs encoding human JNK1 $\alpha$ 1 and JNK1 $\beta$ 1 (i.e., GenBank accession Nos. L26318 and 5 U35004, respectively). ISIS 21862 (SEQ ID NO:116) is complementary to bases 294 to 313 of the human JNK1 $\alpha$ 1 and JNK1 $\beta$ 1 cDNAs (GenBank accession Nos. L26318 and U35004, respectively), bases 289 to 308 of the human JNK1 $\beta$ 2 cDNA (GenBank accession No. U35005), and bases 288 to 307 of the 10 human JNK1 $\alpha$ 2 cDNA (GenBank accession No. U34822). Finally, ISIS 21865 is complementary to bases 654 to 673 of the human JNK1 $\alpha$ 1 cDNA (GenBank accession No. L26318) and to bases 648 to 667 of the human JNK1 $\alpha$ 2 cDNA (GenBank accession No. U34822). These oligonucleotides are tested 15 for their ability to modulate mRNA levels of human JNK1 genes according to the methods described in Example 3.

**TABLE 20: Activities of Oligonucleotides  
Targeted to Rat JNK1**

20	<b>ISIS No:</b>	<b>SEQ ID NO:</b>	<b>GENE TARGET REGION</b>	<b>% EXPRESSION JNK1</b>	<b>% EXPRESSION JNK2</b>
	control <sup>1</sup>	---	---	100%	100%
	21857	111	5'-UTR	24%	91%
	21858	112	5'-UTR	8%	89%
	21859	113	tIR	5%	106%
25	21860	114	ORF	8%	98%
	21861	115	ORF	6%	13%
	21862	116	ORF	6%	133%

- 117 -

20	<b>ISIS</b>	<b>SEQ ID</b>	<b>GENE</b>	%	%
	<b>No:</b>	<b>NO:</b>	<b>TARGET</b>	<b>EXPRESSION</b>	<b>EXPRESSION</b>
			<b>REGION</b>	<b>JNK1</b>	<b>JNK2</b>
	21863	117	ORF	24%	107%
	21864	119	ORF	8%	106%
	21865	119	ORF	5%	50%
	21866	120	ORF	8%	98%
5	21867	121	ORF	5%	21%
	21868	122	ORF	15%	112%
	21869	123	ORF	30%	93%
	21870	124	ORF	11%	87%

<sup>1</sup> Cells treated with LIPOFECTIN™ only (no oligonucleotide).

10           **B. JNK2:** Table 21 describes the sequences and structures of a set of oligonucleotides, ISIS Nos. 18254 to 18267 (SEQ ID NOS:125 to 138, respectively) that were designed to be specifically hybridizable to nucleic acids that encode a stress-activated protein kinase from *Rattus norvegicus* that encode a stress-activated protein kinase named "p54α" or "SAPKα" (Kyriakis et al., *Nature*, 1994, 369, 156). The structures of three control oligonucleotides, ISIS Nos. 21914 to 21916 (SEQ ID NOS:139 to 141, respectively) are also shown in the table. Two 15 isoforms of p54α have been described: "p54α1" (GenBank accession No. L27112, locus name "RATSAPKA") and "p54α2" (GenBank accession No. L27111, locus name "RATSAPKB"). With the exception of ISIS 18257 (SEQ ID NO:128), the 20 oligonucleotides described in Table 21 are specifically hybridizable to nucleic acids encoding either p54α1 or p54α2. ISIS 18257 is specifically hybridizable to nucleic 25

- 118 -

acids encoding p54 $\alpha$ 2 (i.e., GenBank accession No. L27112, locus name "RATSAPKB"). In Table 21, emboldened residues are 2'-methoxyethoxy-residues (others are 2'-deoxy-); "C" residues are 2'-methoxyethoxy-5-methyl-cytosines and "C" 5 residues are 5-methyl-cytosines; "o" indicates a phosphodiester linkage; and "s" indicates a phosphorothioate linkage. The target gene co-ordinates are from GenBank Accession No. L27112, locus name "RATSAPKB."

TABLE 21: Nucleotide Sequences of Rat JNK2 Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE (5' -> 3')	SEQ ID NO:	TARGET NUCLEOTIDE CO-ORDINATES	GENE TARGET	REGION
18254	<b>T</b> <b>C</b> <b>O</b> <b>A</b> <b>O</b> <b>T</b> <b>O</b> <b>G</b> <b>S</b> <b>A</b> <b>T</b> <b>s</b> <b>G</b> <b>T</b> <b>s</b> <b>A</b> <b>S</b> <b>G</b> <b>T</b> <b>s</b> <b>G</b> <b>T</b> <b>s</b> <b>C</b> <b>s</b> <b>A</b> <b>s</b> <b>T</b> <b>T</b> <b>O</b> <b>A</b> <b>O</b> <b>A</b>	125	0001-0020	tir	
18255	<b>T</b> <b>o</b> <b>G</b> <b>O</b> <b>T</b> <b>G</b> <b>s</b> <b>T</b> <b>s</b> <b>G</b> <b>s</b> <b>A</b> <b>s</b> <b>C</b> <b>s</b> <b>A</b> <b>s</b> <b>T</b> <b>T</b> <b>O</b> <b>T</b> <b>O</b> <b>A</b> <b>O</b>	126	0281-0300	ORF	
18256	<b>C</b> <b>o</b> <b>C</b> <b>A</b> <b>O</b> <b>T</b> <b>O</b> <b>A</b> <b>s</b> <b>T</b> <b>s</b> <b>G</b> <b>s</b> <b>A</b> <b>s</b> <b>T</b> <b>s</b> <b>A</b> <b>s</b> <b>C</b> <b>s</b> <b>C</b> <b>s</b> <b>T</b> <b>s</b> <b>G</b> <b>s</b> <b>A</b> <b>T</b> <b>O</b> <b>O</b> <b>C</b> <b>O</b> <b>T</b>	127	0361-0380	ORF	
18257	<b>G</b> <b>o</b> <b>A</b> <b>O</b> <b>T</b> <b>O</b> <b>A</b> <b>T</b> <b>s</b> <b>C</b> <b>s</b> <b>A</b> <b>s</b> <b>C</b> <b>s</b> <b>A</b> <b>s</b> <b>T</b> <b>s</b> <b>C</b> <b>s</b> <b>T</b> <b>s</b> <b>C</b> <b>s</b> <b>T</b> <b>s</b> <b>G</b> <b>T</b> <b>O</b> <b>G</b> <b>T</b>	128	0621-0640	ORF	
18258	<b>G</b> <b>o</b> <b>C</b> <b>O</b> <b>T</b> <b>O</b> <b>C</b> <b>s</b> <b>G</b> <b>s</b> <b>T</b> <b>s</b> <b>C</b> <b>s</b> <b>A</b> <b>s</b> <b>C</b> <b>s</b> <b>A</b> <b>s</b> <b>G</b> <b>s</b> <b>A</b> <b>s</b> <b>G</b> <b>s</b> <b>A</b> <b>T</b> <b>O</b> <b>C</b> <b>O</b> <b>G</b>	129	0941-0960	ORF	
18259	<b>G</b> <b>o</b> <b>C</b> <b>O</b> <b>T</b> <b>O</b> <b>C</b> <b>s</b> <b>G</b> <b>s</b> <b>T</b> <b>s</b> <b>G</b> <b>s</b> <b>A</b> <b>s</b> <b>T</b> <b>s</b> <b>G</b> <b>s</b> <b>A</b> <b>s</b> <b>T</b> <b>s</b> <b>G</b> <b>s</b> <b>A</b> <b>T</b> <b>O</b> <b>G</b> <b>O</b> <b>A</b> <b>G</b>	130	1201-1220	ORF	
18260	<b>A</b> <b>T</b> <b>O</b> <b>C</b> <b>O</b> <b>T</b> <b>O</b> <b>G</b> <b>s</b> <b>C</b> <b>s</b> <b>A</b> <b>s</b> <b>G</b> <b>s</b> <b>T</b> <b>s</b> <b>T</b> <b>s</b> <b>C</b> <b>s</b> <b>A</b> <b>s</b> <b>T</b> <b>T</b> <b>O</b> <b>C</b> <b>O</b> <b>G</b> <b>O</b> <b>C</b>	131	1281-1300	ttr	
18261	<b>C</b> <b>o</b> <b>C</b> <b>A</b> <b>O</b> <b>C</b> <b>C</b> <b>s</b> <b>A</b> <b>s</b> <b>G</b> <b>s</b> <b>C</b> <b>s</b> <b>T</b> <b>s</b> <b>C</b> <b>s</b> <b>C</b> <b>s</b> <b>A</b> <b>s</b> <b>T</b> <b>s</b> <b>G</b> <b>s</b> <b>T</b> <b>O</b> <b>G</b> <b>O</b> <b>C</b> <b>O</b> <b>T</b> <b>O</b> <b>C</b>	132	1341-1360	3'-UTR	
18262	<b>C</b> <b>o</b> <b>A</b> <b>O</b> <b>G</b> <b>O</b> <b>T</b> <b>O</b> <b>T</b> <b>s</b> <b>A</b> <b>s</b> <b>C</b> <b>s</b> <b>A</b> <b>s</b> <b>T</b> <b>s</b> <b>G</b> <b>s</b> <b>A</b> <b>s</b> <b>T</b> <b>T</b> <b>O</b> <b>T</b> <b>C</b> <b>s</b> <b>T</b> <b>O</b> <b>G</b> <b>O</b> <b>C</b> <b>O</b> <b>T</b> <b>O</b> <b>C</b>	133	1571-1590	3'-UTR	
18263	<b>A</b> <b>A</b> <b>O</b> <b>G</b> <b>O</b> <b>A</b> <b>O</b> <b>G</b> <b>s</b> <b>A</b> <b>s</b> <b>T</b> <b>s</b> <b>A</b> <b>s</b> <b>G</b> <b>s</b> <b>A</b> <b>s</b> <b>G</b> <b>s</b> <b>A</b> <b>s</b> <b>T</b> <b>T</b> <b>O</b> <b>A</b> <b>O</b> <b>T</b> <b>O</b> <b>T</b>	134	1701-1720	3'-UTR	
18264	<b>A</b> <b>o</b> <b>G</b> <b>O</b> <b>C</b> <b>O</b> <b>A</b> <b>O</b> <b>G</b> <b>s</b> <b>A</b> <b>s</b> <b>G</b> <b>s</b> <b>T</b> <b>s</b> <b>G</b> <b>s</b> <b>A</b> <b>s</b> <b>A</b> <b>s</b> <b>T</b> <b>s</b> <b>A</b> <b>s</b> <b>C</b> <b>s</b> <b>A</b> <b>o</b> <b>A</b> <b>c</b> <b>O</b> <b>T</b> <b>O</b> <b>T</b>	135	2001-2020	3'-UTR	

- 120 -

ISIS NO.	NUCLEOTIDE SEQUENCE (5' -> 3')	SEQ ID	TARGET NUCLEOTIDE NO: CO-ORDINATES	GENE TARGET REGION
18265	<b>T</b> o <b>G</b> o <b>T</b> o <b>C</b> o <b>A</b> s <b>G</b> c <b>C</b> st <b>C</b> st <b>T</b> as <b>A</b> sc <b>S</b> as <b>T</b> st <b>s</b> a <b>o</b> g <b>o</b> co <b>A</b>	136	2171-2190	3'-UTR
18266	<b>A</b> o <b>G</b> o <b>T</b> o <b>A</b> o <b>A</b> s <b>G</b> c <b>C</b> cs <b>C</b> st <b>C</b> st <b>T</b> sc <b>G</b> s <b>G</b> t <b>O</b> to <b>A</b> o <b>G</b>	137	2371-2390	3'-UTR
18267	<b>A</b> o <b>A</b> o <b>A</b> o <b>T</b> o <b>G</b> s <b>G</b> as <b>A</b> as <b>A</b> as <b>G</b> sc <b>S</b> as <b>G</b> sc <b>S</b> as <b>G</b> co <b>A</b> o <b>G</b> o <b>C</b>	138	2405-2424	3'-UTR
21914	<b>G</b> o <b>C</b> o <b>T</b> o <b>C</b> o <b>A</b> s <b>G</b> t <b>s</b> g <b>s</b> as <b>T</b> as <b>S</b> as <b>T</b> g <b>s</b> a <b>o</b> t <b>O</b> g <b>o</b> ao <b>G</b>	139	18259 control	---
21915	<b>G</b> o <b>C</b> o <b>T</b> o <b>A</b> o <b>A</b> s <b>G</b> c <b>C</b> gs <b>G</b> st <b>T</b> sc <b>S</b> as <b>S</b> as <b>G</b> st <b>O</b> to <b>O</b> g <b>o</b> ao <b>G</b>	140	18259 control	---
21916	<b>G</b> o <b>C</b> o <b>T</b> o <b>C</b> o <b>G</b> s <b>G</b> t <b>s</b> g <b>s</b> as <b>A</b> as <b>T</b> g <b>s</b> g <b>s</b> a <b>o</b> t <b>O</b> co <b>A</b> o <b>G</b>	141	18259 control	---

- 121 -

**TABLE 22:**  
**Activities of Oligonucleotides Targeted to Rat JNK2**

	<b>ISIS No:</b>	<b>SEQ ID NO:</b>	<b>GENE TARGET REGION</b>	<b>% EXPRESSION</b>	<b>% INHIBITION</b>
5	control <sup>1</sup>	---	---	100%	0%
	18254	125	tIR	20%	80%
	18255	126	ORF	21%	79%
	18256	127	ORF	80%	20%
	18257	128	ORF	32%	68%
10	18259	129	ORF	19%	81%
	18259	130	ORF	15%	68%
	18260	131	ORF	41%	59%
	18261	132	3'-UTR	47%	0%
	18262	133	3'-UTR	50%	50%
15	18263	134	3'-UTR	63%	37%
	18264	135	3'-UTR	48%	52%
	18265	136	3'-UTR	38%	62%
	18266	137	3'-UTR	66%	34%
	18267	138	3'-UTR	84%	16%

20 <sup>1</sup> Cells treated with LIPOFECTIN™ only (no oligonucleotide).

These antisense compounds were tested for their ability to modulate levels of p54 $\alpha$  (JNK2) mRNA in A10 cells using the radiolabeled human JNK2 cDNA as a probe as described *supra*. The results are shown in Table 22.

- 122 -

Oligonucleotides showing levels of inhibition from  $\geq$  about 60% to about 100% of rat JNK2 mRNA levels include ISIS Nos. 18254, 18255, 18257, 18258, 18259, 18260 and 18264 (SEQ ID NOS:125, 126, 128, 129, 130, 131 and 135, respectively).

- 5 These oligonucleotides are preferred embodiments of the invention for modulating rat JNK2 expression.

Oligonucleotides showing levels of inhibition of from  $\geq$  about 80% to about 100% of rat JNK1 mRNAs in this assay include ISIS Nos. 18254, 18255, 18258 and 18259 (SEQ ID

- 10 NOS:125, 126, 129 and 130, respectively). These oligonucleotides are thus more preferred embodiments of the invention for modulating rat JNK2 expression. ISIS 18259 (SEQ ID NO:130) was chosen for use in further studies (*infra*).

- 15       **C. Dose Response:** A dose response study was conducted using oligonucleotides targeted to rat JNK1 (ISIS 21859; SEQ ID NO:113) and JNK2 (ISIS 18259; SEQ ID NO:130) and Northern assays. The results (Table 23) demonstrate an increasing effect as the oligonucleotide concentration is  
20 raised and confirm that ISIS Nos. 21859 and 18259 (SEQ ID NOS:113 and 130, respectively) specifically modulate levels of mRNA encoding JNK1 and JNK2, respectively.

- 123 -

**TABLE 23:**  
**Dose-Dependent Response to Rat JNK**  
**Antisense Oligonucleotides (ASOs)**

ISIS #	SEQ ID NO:	ASO Description	Dose	% EXPRESSION JNK1	% EXPRESSION JNK2
5	21859	rat JNK1 active ASO	0 nM	100	100
			10 nM	74	101
			50 nM	25	98
			100 nM	11	99
			200 nM	8	101
10	18259	rat JNK2 active ASO	0 nM	100	10
			10 nM	95	81
			50 nM	101	35
			100 nM	94	15
			200 nM	89	5

D. JNK3: Table 24 describes the sequences and structures of a set of oligonucleotides, ISIS Nos. 21899 to 21912 (SEQ ID NOS:142 to 155, respectively) that were 10 designed to be specifically hybridizable to nucleic acids from *Rattus norvegicus* that encode a stress-activated protein kinase named "p54 $\beta$ " that is homologous to the human protein JNK3 (Kyriakis et al., *Nature*, 1994, 369, 156; GenBank accession No. L27128, locus name "RATSAPC"). In 15 Table 24, emboldened residues are 2'-methoxyethoxy-residues (others are 2'-deoxy-); "C" residues are 2'-methoxyethoxy-5-methyl-cytosines and "C" residues are 5-methyl-cytosines; "o" indicates a phosphodiester linkage; and "s" indicates a phosphorothioate linkage. The target gene co-ordinates are

- 124 -

from GenBank Accession No. L27128, locus name "RATSAPKC." The oligonucleotides are tested for their ability to modulate rat JNK3 mRNA levels essentially according to the methods described in the preceding Examples.

5        In addition to being specifically hybridizable to nucleic acids encoding rat JNK3, some of the oligonucleotides described in Table 24 are also specifically hybridizable with JNK3-encoding nucleic acids from humans and *Mus musculus* (mouse). Table 25 sets out  
10 these relationships. These oligonucleotides are tested for their ability to modulate mRNA levels of the human JNK genes according to the methods described in Example 5.

TABLE 24: Nucleotide Sequences of Rat JNK3 Oligonucleotides

ISIS NO.	NUCLEOTIDE SEQUENCE (5' -> 3')	SEQ NO:	TARGET ID NUCLEOTIDE CO-ORDINATES	GENE TARGET REGION
21899	GoGoGoCotsTstsCsAsTsTstsAsGscsCsAaCoAtoT	142	0021-0040	5'-UTR
21900	GoGoToToGsGstsCsAsCstsGscsAsGotoAgoToT	143	0241-0260	5'-UTR
21901	ToGoCoToCsAsTsGstsTsAsAsTsGotoToToG	144	0351-0370	TIR
21902	GoToCoGoAsGsAsCsAsGsGsTsCsAtoAoCoG	145	0491-0510	ORF
21903	CoGoAoCoAsTsCscGsCstsGsGotoCoCoA	146	0731-0750	ORF
21904	AoCoAtoAoCsGsAsGsAsTsCsAsTsCsAtoGooAoA	147	0901-0920	ORF
21905	GoCoAoAoTstsCstsCsAsTsGsAsAtoToCoT	148	1101-1120	ORF
21906	ToCoGotoAAsCsAsAsCsGstsTsGsAtoGotoA	149	1321-1340	ORF
21907	CoGoCoGsAsGsGsCsTsTsCsAsGsgCoToGoc	150	1601-1620	ORF
21908	GoGoCotoAsGsTsCsAsCsCsTsGsCsAsAaCoAoC	151	1631-1650	tTR

- 126 -

ISIS NO.	NUCLEOTIDE SEQUENCE (5' -> 3')	SEQ ID NO: CO-ORDINATES	TARGET GENE	GENE TARGET REGION
21909	GCGCTGGGCGGTTGGCGT	152	1771-1790	3'-UTR
21910	GCGCTGGGCGGTTGGCGT	153	1891-1910	3'-UTR
21911	AAGGGGAAACGGGAAAGGTT	154	1921-1940	3'-UTR
21912	AAGGGGAAACGGGAAAGGTT	155	1941-1960	3'-UTR

- 127 -

**TABLE 25: Cross-Hybridizations of Rat JNK3 Oligonucleotides**

ISIS NO.	SEQ ID NO:	Hybridizes to:		
		Human JNK3a1 <sup>1</sup>	Human JNK3a2 <sup>2</sup>	Mouse JNK3 <sup>3</sup>
5	21900	143	---	---
	21901	143	bp 193-212	bp 169-188
	21904	147	---	bp 961-980
	21905	148	bp 943-962	bp 919-938
	21906	149	---	---
	21908	151	bp 1478-1497	bp 1449-1468
				bp 1696-1715

10 <sup>1</sup> GenBank accession No. U34820, locus name "HSU34820" (see also Mohit et al., *Neuron*, 1995, 14, 67 and Gupta et al., *EMBO Journal*, 1996, 15, 2760).

<sup>2</sup> GenBank accession No. U34819, locus name "HSU34819" (see also Gupta et al., *EMBO Journal*, 1996, 15, 2760).

15 <sup>3</sup> Also known as p45<sup>3F12</sup> MAPK; GenBank accession No. L35236, locus name "MUSMAPK" (see also Martin et al., *Brain Res. Mol. Brain Res.*, 1996, 35, 47).

**E. Pan JNK Oligonucleotides:** Certain of the oligonucleotides of the invention are capable of modulating 20 two or more JNK proteins and are referred to herein as "Pan JNK" oligonucleotides. For example, ISIS Nos. Nos. 21861 and 21867 (SEQ ID NOS:115 and 121, respectively)

demonstrated a capacity to modulate both JNK1 and JNK2 (Table 20). Such oligonucleotides are useful when the concomitant modulation of several JNK proteins is desired.

Human Pan JNK oligonucleotides are described in 5 Table 26. These oligonucleotides are designed to be complementary to sequences that are identically conserved in (i.e., SEQ ID NOS:156, 158, 159, 160 and 161), or which occur with no more than a one-base mismatch (SEQ ID NO:157), in nucleic acids encoding human JNK1 $\alpha$ 1, JNK1 $\alpha$ 2, 10 JNK2 $\alpha$ 1 and JNK2 $\alpha$ 2. The oligonucleotides described in Table 26 are evaluated for their ability to modulate JNK1 and JNK2 mRNA levels in A549 cells using the methods and assays described in Examples 3 and 4.

In instances where such common sequences 15 encompass one or more base differences between the JNK genes that it is desired to modulate, hypoxanthine (inosine) may be incorporated at the positions of the oligonucleotide corresponding to such base differences. ("Hypoxanthine" is the art-accepted term for the base that 20 corresponds to the nucleoside inosine; however, the term "inosine" is used herein in accordance with U.S. and PCT rules regarding nucleotide sequences.) As is known in the art, inosine (I) is capable of hydrogen bonding with a variety of nucleobases and thus serves as a "universal" 25 base for hybridization purposes. For example, an oligonucleotide having a sequence that is a derivative of SEQ ID NO:157 having one inosine substitution (TAGGAIATTCTTCATGATC, SEQ ID NO:162) is predicted to bind to nucleic acids encoding human JNK1 $\alpha$ 1, JNK1 $\alpha$ 2, JNK2 $\alpha$ 1 and 30 JNK2 $\alpha$ 2 with no mismatched bases. As another example, an oligonucleotide having a sequence that is a derivative of SEQ ID NO:161 having one inosine substitution (GGTTGCAITTTCTTCATGAA, SEQ ID NO:163) is predicted to bind

- 129 -

with no mismatched bases to nucleic acids encoding human JNK3 $\alpha$ 1 and JNK3 $\alpha$ 2 in addition to JNK1 $\alpha$ 1, JNK1 $\alpha$ 2, JNK2 $\alpha$ 1 and JNK2 $\alpha$ 2. Such oligonucleotides are evaluated for their ability to modulate JNK1 and JNK2 mRNA levels in A549 5 cells, and JNK3 mRNA levels in SH-SY5Y cells, using the methods and assays described in Examples 3, 4 and 5.

**TABLE 26: Human Pan JNK Oligonucleotides**

	NUCLEOTIDE SEQUENCE (5' -> 3') AND CHEMICAL MODIFICATIONS*	SEQ ID NO:
10	<b>A<sup>s</sup>C<sup>s</sup>T<sup>s</sup>C<sup>s</sup>T<sup>s</sup>T<sup>0</sup>G<sup>0</sup>A<sup>0</sup>A<sup>0</sup>T<sup>0</sup>T<sup>0</sup>C<sup>s</sup>T<sup>s</sup>C<sup>s</sup>T<sup>s</sup>A<sup>s</sup>G</b>	156
	<b>T<sup>s</sup>A<sup>s</sup>G<sup>s</sup>S<sup>s</sup>T<sup>s</sup>A<sup>0</sup>T<sup>0</sup>T<sup>0</sup>C<sup>0</sup>T<sup>0</sup>T<sup>0</sup>C<sup>s</sup>A<sup>s</sup>T<sup>s</sup>G<sup>s</sup>A<sup>s</sup>T<sup>s</sup>C</b>	157
	<b>A<sup>s</sup>G<sup>s</sup>A<sup>s</sup>G<sup>s</sup>G<sup>s</sup>T<sup>0</sup>A<sup>0</sup>G<sup>0</sup>G<sup>0</sup>A<sup>0</sup>C<sup>0</sup>A<sup>0</sup>T<sup>s</sup>C<sup>s</sup>T<sup>s</sup>T<sup>s</sup>T<sup>s</sup>C</b>	158
	<b>T<sup>s</sup>T<sup>s</sup>A<sup>s</sup>T<sup>s</sup>T<sup>s</sup>C<sup>0</sup>C<sup>0</sup>A<sup>0</sup>C<sup>0</sup>T<sup>0</sup>G<sup>0</sup>A<sup>0</sup>T<sup>s</sup>C<sup>s</sup>A<sup>s</sup>S<sup>s</sup>S<sup>s</sup>S<sup>s</sup>T<sup>s</sup>A<sup>s</sup>T<sup>s</sup></b>	159
	<b>T<sup>s</sup>C<sup>s</sup>A<sup>s</sup>T<sup>s</sup>A<sup>s</sup>C<sup>0</sup>T<sup>0</sup>T<sup>0</sup>A<sup>0</sup>T<sup>0</sup>T<sup>0</sup>C<sup>s</sup>C<sup>s</sup>A<sup>s</sup>C<sup>s</sup>T<sup>s</sup>G</b>	160
15	<b>G<sup>s</sup>G<sup>s</sup>T<sup>s</sup>G<sup>s</sup>C<sup>s</sup>A<sup>0</sup>G<sup>0</sup>T<sup>0</sup>T<sup>0</sup>T<sup>0</sup>C<sup>0</sup>T<sup>0</sup>T<sup>0</sup>S<sup>s</sup>C<sup>s</sup>A<sup>s</sup>T<sup>s</sup>G<sup>s</sup>A<sup>s</sup>A</b>	161

\*Emboldened residues, 2'-methoxyethoxy- residues (others are 2'-deoxy-); all "C" residues are 5-methyl-cytosines; "0", phosphodiester linkage; "s", phosphorothioate linkage.

- 130 -

**What is claimed is:**

1. An oligonucleotide comprising from 8 to 30 nucleotides connected by covalent linkages, wherein said oligonucleotide has a sequence specifically hybridizable 5 with a nucleic acid encoding a JNK1 protein, wherein said oligonucleotide modulates the expression of said JNK1 protein and wherein said oligonucleotide is not specifically hybridizable to the start codon of said nucleic acid encoding said JNK1 protein.

10 2. An oligonucleotide comprising from 8 to 30 nucleotides connected by covalent linkages, wherein said oligonucleotide has a sequence specifically hybridizable to the start codon of a nucleic acid encoding a JNK1 protein and wherein said oligonucleotide modulates the expression 15 of said JNK1 protein and wherein said sequence is SEQ ID NO:13.

3. An oligonucleotide comprising from 8 to 30 nucleotides connected by covalent linkages, wherein said oligonucleotide has a sequence specifically hybridizable 20 with a nucleic acid encoding a JNK2 protein and wherein said oligonucleotide modulates the expression of said JNK2 protein.

4. An oligonucleotide comprising from 8 to 30 nucleotides connected by covalent linkages, wherein said 25 oligonucleotide has a sequence specifically hybridizable with a nucleic acid encoding a JNK3 protein and wherein said oligonucleotide modulates the expression of said JNK3 protein.

- 131 -

5. The oligonucleotide of any one of claims 1 to  
4, wherein at least one of said covalent linkages of said  
oligonucleotide is a modified covalent linkage.

6. The oligonucleotide of any one of claims 1 or  
5 5, wherein at least one of said nucleotides has a modified  
nucleobase.

7. The oligonucleotide of claim 6 wherein said  
modified nucleobase is 5-methylcytosine.

8. The oligonucleotide of any one of claims 1 to  
10 7, wherein at least one of said nucleotides has a modified  
sugar moiety.

9. The oligonucleotide of claim 8 having at  
least two non-contiguous nucleotides having modified sugar  
moieties.

15 10. The oligonucleotide of either of claims 8 or  
9 wherein said modified sugar moiety is a 2'-modified sugar  
moiety.

11. The oligonucleotide of claim 10 wherein said  
2'-modified sugar moiety is a 2'-methoxyethoxy modified  
20 sugar moiety.

12. The oligonucleotide of any one of claims 1 to  
11 further comprising at least one lipophilic moiety which  
enhances the cellular uptake of said oligonucleotide.

- 132 -

13. The oligonucleotide of any one of claims 1 to 12 wherein said oligonucleotide has a sequence specifically hybridizable with two or more nucleic acids encoding different isoforms of a JNK protein and wherein said 5 oligonucleotide modulates the expression of said two or more isoforms of said JNK protein.

14. The oligonucleotide of any one of claims 1 to 12 wherein said oligonucleotide has a sequence specifically hybridizable with a nucleic acid encoding a first isoform 10 of a JNK protein, and said sequence of said oligonucleotide is not specifically hybridizable with a nucleic acid encoding a second isoform of said JNK protein, and wherein said oligonucleotide modulates the expression of said first isoform of said JNK protein but not that of said second 15 isoform of said JNK protein.

15. The oligonucleotide of any one of claims 1 to 14 wherein said JNK protein is that of a mammal.

16. A method of modulating the expression of a JNK protein in cells or tissues comprising contacting said 20 cells or tissues with the oligonucleotide of any one of claims 1 to 15.

17. A method of modulating cell cycle progression in cultured cells or the cells of an animal comprising administering to said cells an effective amount of the 25 oligonucleotide of any one of claims 1 to 15.

18. A method of modulating, in cultured cells or the cells of an animal, the phosphorylation of a protein

- 133 -

phosphorylated by a JNK protein, wherein said method comprises administering to said cells an effective amount of the oligonucleotide of any one of claims 1 to 15.

19. A method of modulating, in cultured cells or  
5 the cells of an animal, the expression of a cellular protein that promotes one or more metastatic events, wherein said method comprises administering to said cells an effective amount of the oligonucleotide of any one of claims 1 to 15.

10 20. A pharmaceutical composition comprising the oligonucleotide of any one of claims 1 to 15, or a bioequivalent thereof, and a pharmaceutically acceptable carrier.

21. The pharmaceutical composition of claim 20,  
15 further comprising one or more compounds from the list consisting of a stabilizing agent, a penetration enhancer, a carrier compound and a chemotherapeutic agent.

22. A pharmaceutical composition comprising a plurality of the oligonucleotides of any one of claims 1 to  
20 15, or bioequivalents thereof, and a pharmaceutically acceptable carrier.

23. A method of treating an animal having, suspected of having or prone to having a hyperproliferative disease comprising administering to said animal a prophylactically or therapeutically effective amount of the pharmaceutical composition of any one of claims 20 to 22.

- 134 -

24. A method of inhibiting the growth of a tumor in an animal comprising administering to said animal an effective amount of the pharmaceutical composition of any one of claims 20 to 22.

## SEQUENCE LISTING

<110> McKay, Robert A.  
Dean, Nicholas M.  
Monia, Brett  
Nero, Pam  
Gaarde, William A.

<120> ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS FOR THE  
MODULATION OF JNK PROTEINS

<130> ISPH-0314

<150> 08/910,629  
<151> 1997-08-03

<160> 161

<210> 1  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 1  
attctttcca ctcttctatt 20

<210> 2  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 2  
ctcctccaag tccataactt 20

<210> 3  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 3  
cccgtaaac tccatttttg 20

<210> 4  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 4  
ctgtgctaaa ggagagggct 20

<210> 5  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 5  
atgatggatg ctgagagcca 20

<210> 6

<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 6  
gttgacattg aagacacatc 20

<210> 7  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 7  
ctgtatcaga ggccaaagtc 20

<210> 8  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 8  
tgctgcttct agactgctgt 20

<210> 9  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 9  
agtcatctac agcagccag 20

<210> 10  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 10  
ccatccctcc caccccccga 20

<210> 11  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 11  
atcaatgact aaccgactcc 20

<210> 12  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 12

caaaaataag accactgaat 20

<210> 13  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 13  
cacgcttgct tctgctcatg 20

<210> 14  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 14  
cggttagct tcttgattgc 20

<210> 15  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 15  
cccgcttggc atgagtctga 20

<210> 16  
<211> 20

<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 16  
ctctctgttag gcccgcttgg

20

<210> 17  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 17  
atttgcatcc atgagactcca

20

<210> 18  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 18  
cgttcctgca gtcctggcca

20

<210> 19  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 19

ggatgacctc gggtgctctg

20

<210> 20

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 20

cccatatatgc accccacaga

20

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 21

cgggtgttgg agagttcat

20

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 22

ttaggtggtg gagcttctgc

20

<210> 23  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 23  
ggctgcccccc gataactcc

20

<210> 24  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 24  
tgctaaagga gagggctgcc

20

<210> 25  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 25  
aggccaaagt cggatctgtt

20

<210> 26  
<211> 20  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; antisense sequence

&lt;400&gt; 26

ccaccccccgg atggcccaag

20

&lt;210&gt; 27

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; control sequence (sense)

&lt;400&gt; 27

ccaagcgggc ctacagagag

20

&lt;210&gt; 28

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; control sequence (scrambled)

&lt;400&gt; 28

ctttccgttg gaccctggg

20

&lt;210&gt; 29

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; antisense sequence

&lt;400&gt; 29

gtttcagatc cctcgccccgc 20  
  
<210> 30  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> antisense sequence  
  
<400> 30  
tgca~~g~~cacaa acaatccctt 20  
  
<210> 31  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> antisense sequence  
  
<400> 31  
gtccgggcca ggccaa~~g~~tgc 20  
  
<210> 32  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> antisense sequence  
  
<400> 32  
caggatgact tcgggccc 20  
  
<210> 33  
<211> 20

<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 33  
gctctcccat gatgcaaccc

20

<210> 34  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 34  
atgggtgacg cagagcttcg

20

<210> 35  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 35  
ctgctgcattc tgaaggctga

20

<210> 36  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 36

tgagaaggag tggcgttgct

20

<210> 37

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 37

tgctgtctgt gtctgaggcc

20

<210> 38

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 38

ggtcccgatcg aggcatacaag

20

<210> 39

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 39

catttcaggc ccacggaggt

20

<210> 40  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 40  
ggtctgaata gggcaaggca 20

<210> 41  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 41  
gggcaagtcc aagcaaggcat 20

<210> 42  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence (sense)

<400> 42  
gactttggcc tggcccgac 20

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>

<223> control sequence (scrambled)

<400> 43

gtgcgcgcga gcccgaaatc 20

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 44

tcaaacagtt tcttgataa 20

<210> 45

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 45

ctcatctata ggaaacgggt 20

<210> 46

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 46

tggaggctca taaataccac 20

<210> 47  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 47  
tataagaaat ggaggctcat 20

<210> 48  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 48  
tcacatccaa tgttggttca 20

<210> 49  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 49  
ttatcgaatc cctgacaaaa 20

<210> 50  
<211> 20

<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 50  
gtttggcaat atatgacaca

20

<210> 51  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 51  
ctgtcaagga cagcatcata

20

<210> 52  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 52  
aatcacttga cataagttgg

20

<210> 53  
<211> 20  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

<223> antisense sequence

<400> 53

taaatccctg tgaataattc

20

<210> 54

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 54

gcatccccaca gaccatatat

20

<210> 55

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 55

tgttctcttt catccaaactg

20

<210> 56

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 56

tctcaactgct gttcaactgct

20

<210> 57  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 57  
gggtctggtc ggtggacatg

20

<210> 58  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 58  
aggctgctgt cagtgtcaga

20

<210> 59  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 59  
tcacctgcaa caacccaggg

20

<210> 60  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 60  
gcggctagtc acctgcaaca 20

<210> 61  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 61  
cgctgggttt cgcgaggcagg 20

<210> 62  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 62  
atcatctcct gaagaacgct 20

<210> 63  
<211> 35  
<212> DNA  
<213> Homo Sapiens

<300>  
<308> L26318 Genbank  
<309> 1994-04-25  
<313> FROM 631 TO 665

<300>  
<308> U34822 Genbank  
<309> 1996-07-26  
<313> FROM 625 TO 659

<400> 63  
aacgtggatt tatggtctgt ggggtgcatt atggg

35

<210> 64  
<211> 35  
<212> DNA  
<213> Homo sapiens

<300>  
<308> U35004 Genbank  
<309> 1996-07-26  
<313> FROM 631 TO 665

<300>  
<308> U35005 Genbank  
<309> 1996-07-26  
<313> FROM 626 TO 660

<400> 64  
aacgttgaca tttggtcagt tgggtgcatt atggg

35

<210> 65  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> reverse complement of SEQ ID NO. 63

<400> 65  
cccataatgc accccacaga ccataaatcc acgtt

35

<210> 66  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> reverse complement of SEQ ID NO. 64

<400> 66  
cccatgatgc acccaactga ccaaatgtca acgtt 35

<210> 67  
<211> 44  
<212> DNA  
<213> Homo sapiens

<300>  
<308> L26318 Genbank  
<309> 1994-04-25  
<313> FROM 668 TO 711

<300>  
<308> U34822 Genbank  
<309> 1996-07-26  
<313> FROM 662 TO 705

<400> 67  
aatggtttg ccacaaaatc ctcttccag gaagggacta tatt 44

<210> 68  
<211> 44  
<212> DNA  
<213> Homo sapiens

<300>  
<308> U35004 Genbank  
<309> 1996-07-26

<313> FROM 668 TO 711

<300>

<308> U35005 Genbank

<309> 1996-07-26

<313> FROM 663 TO 706

<400> 68

aatatgatcaa aggtgggtt ttgttcccag gtacagatca tatt

44

<210> 69

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse complement to SEQ ID NO. 67

<400> 69

aatatacgtcc cttcctggaa agaggatttt gtggcaaacc attt

44

<210> 70

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse complement to SEQ ID NO. 68

<400> 70

aatatgatct gtacctggaa acaaaacacc acctttgatc attt

44

<210> 71

<211> 32

<212> DNA

<213> Homo sapiens

<308> L26318 Genbank  
<309> 1994-04-25  
<313> FROM 1144 TO 1175

<300>  
<308> U35004 Genbank  
<309> 1996-07-26  
<313> FROM 1144 TO 1175

<400> 71  
ccctctcctt tagcacaggt gcagcagtga tc

32

<210> 72  
<211> 27  
<212> DNA  
<213> Homo sapiens

<300>  
<308> U34822 Genbank  
<309> 1996-07-26  
<313> FROM 1138 TO 1164

<300>  
<308> U35005 Genbank  
<309> 1996-07-26  
<313> FROM 1139 TO 1165

<400> 72  
ccctctcctt taggtgcagc agtgatc

27

<210> 73  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> reverse complement to SEQ ID NO. 71

<400> 73  
gatcactgct gcacacctgtgc taaaggagag gg 32

<210> 74  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> reverse complement to SEQ ID NO. 72

<400> 74  
gatcactgct gcacctaag gagaggg 27

<210> 75  
<211> 60  
<212> DNA  
<213> Homo sapiens

<300>  
<308> L31951 Genbank  
<309> 1994-12-06  
<313> FROM 689 TO 748

<300>  
<308> U34821 Genbank  
<309> 1996-07- 26  
<313> FROM 675 TO 734

<400> 75  
gtgggttgca tcatggaga gctggtgaaa gtttgtgtga tattccaagg 50  
cactgaccat 60

<210> 76  
<211> 60  
<212> DNA  
<213> Homo sapiens

&lt;300&gt;

<308> U35002 Genbank  
<309> 1994-07-26  
<313> FROM 653 TO 712

&lt;300&gt;

<308> U35003 Genbank  
<309> 1996-07- 26  
<313> FROM 665 TO 724

&lt;400&gt; 76

gtcgggtgca tcatggcaga aatggtcctc cataaaagtcc tgttccccggg 50  
aagagactat 60

&lt;210&gt; 77

<211> 60  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

<223> reverse complement to SEQ ID NO. 75

&lt;400&gt; 77

atggtcagtg ccttggaaata tcacacaacc tttcaccaggc tctcccatga 50  
tgcaacccac 60

&lt;210&gt; 78

<211> 60  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

<223> reverse complement to SEQ ID NO. 76

&lt;400&gt; 78

atagtctctt cccggaaaca ggactttatg gaggaccatt tctgccatga 50  
tgcacccgac 60

<210> 79  
<211> 35  
<212> DNA  
<213> Homo sapiens

<300>  
<308> U34821 Genbank  
<309> 1996-07- 26  
<313> FROM 1164 TO 1198

<300>  
<308> U35002 Genbank  
<309> 1994-07-26  
<313> FROM 1142 TO 1176

<400> 79  
gatcagccctt cagcacagat gcagcagtaa gtagc

35

<210> 80  
<211> 30  
<212> DNA  
<213> Homo sapiens

<300>  
<308> L31951 Genbank  
<309> 1994-12-06  
<313> FROM 1178 TO 1207

<300>  
<308> U35003 Genbank  
<309> 1996-07- 26  
<313> FROM 1154 TO 1183

<400> 80  
gatcagccctt cagatgcagc agtaagtgc

30

<210> 81

<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> reverse complement to SEQ ID NO. 79

<400> 81  
gctacttact gctgcacatcg tgctgaaggc tgatc 35

<210> 82  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> reverse complement to SEQ ID NO. 80

<400> 82  
gctacttact gctgcacatcg aaggctgatc 30

<210> 83  
<211> 38  
<212> DNA  
<213> Homo sapiens

<300>  
<308> U34820 Genbank  
<309> 1994-07-26  
<313> FROM 1325 TO 1362

<400> 83  
ggacagccctt ctccttcagc acaggtgcag cagtgaac 38

<210> 84  
<211> 33  
<212> DNA

<213> Homo sapiens

<300>

<308> U34819 Genbank

<309> 1994-07-26

<313> FROM 1301 TO 1333

<400> 84

ggacagcctt ctccttcagg tgcagcagtg aac

33

<210> 85

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse complement to SEQ ID NO. 83

<400> 85

gttcaactgct gcacctgtgc tgaaggagaa ggctgtcc

38

<210> 86

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse complement to SEQ ID NO. 84

<400> 86

gttcaactgct gcacctgaag gagaaggctg tcc

33

<210> 87

<211> 20

<212> DNA

<213> Artificial Sequence

<220>  
<223> control sequence

<400> 87  
atgggtgact cagagcttcg 20

<210> 88  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 88  
atgggttact cagagcttcg 20

<210> 89  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 89  
atgggttact catacgcttcg 20

<210> 90  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 90

atgtgttact catagcttcg 20

<210> 91  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 91  
tttgtgttact catagcttcg 20

<210> 92  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 92  
tttgtgttact catagtttcg 20

<210> 93  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 93  
ctgctgcatt tgaaggctga 20

<210> 94  
<211> 20

<212> DNA  
<213> Artificial Sequence  
<220>  
<223> control sequence

<400> 94  
ctgctgcatt tgtaggctga 20

<210> 95  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 95  
ctgctgtatt tgtaggctga 20

<210> 96  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 96  
ctgttgtatt tgtaggctga 20

<210> 97  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 97  
ctgttgtatt tgttagtctga 20

<210> 98  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 98  
tttgttgtatt tgttagtctga 20

<210> 99  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 99  
tgctgtctga gtctgaggcc 20

<210> 100  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 100  
tgctgtatga gtctgaggcc 20

<210> 101

<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 101  
tgctgtatga gtatgaggcc

20

<210> 102  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 102  
tgcagtatga gtatgaggcc

20

<210> 103  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 103  
tgcagtatga gtatgaagcc

20

<210> 104  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 104  
agcagtatga gtatgaagcc 20

<210> 105  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 105  
ggtcccggtct aggcatcaag 20

<210> 106  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 106  
ggtcccattct aggcatcaag 20

<210> 107  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 107

ggttccttctt aggcatcaag 20

<210> 108  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 108  
ggttccttctt agtcatcaag 20

<210> 109  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 109  
ggttccttctt agtcattaaag 20

<210> 110  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 110  
tgttccttctt agtcattaaag 20

<210> 111  
<211> 20

<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 111  
caacgtccccg cgctcgccg

20

<210> 112  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 112  
cctgctcgc ggctccgcgtt

20

<210> 113  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 113  
ctcatgatgg caagcaatta

20

<210> 114  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 114

tgttgtcacg tttacttctg

20

<210> 115

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 115

cggtaggctc gcttagcatg

20

<210> 116

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 116

ctagggattt ctgtggtg

20

<210> 117

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 117

cagcagagtg aagggtgcttg

20

<210> 118  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<400> 118  
tcgttccctgc agtccttgcc

20

<210> 119  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 119  
ccatattctcc cataaatgcac

20

<210> 120  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 120  
tgaattcagg acaaggtgtt

20

<210> 121  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 121  
agcttcgtct acggagatcc 20

<210> 122  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 122  
cactcctcta ttgtgtgctc 20

<210> 123  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 123  
gctgcaccta aaggagacgg 20

<210> 124  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 124  
ccagagtcgg atctgtggac 20

<210> 125

<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 125  
tcatgatgtatgtataca

20

<210> 126  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 126  
tgtgggtgtatgtataacacatttaa

20

<210> 127  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 127  
ccatatgaat aacctgacat

20

<210> 128  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 128

gatatcaaca ttctccttgt 20

<210> 129

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 129

gtttcgtcca cagagatccg 20

<210> 130

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 130

gctcagtggaa catggatgag 20

<210> 131

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 131

atctgcgagg tttcatcgcc 20

<210> 132  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 132  
ccaccagctc ccatgtgctc 20

<210> 133  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 133  
cagttacaca tgatctgtca 20

<210> 134  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 134  
aagaggatta agagattatt 20

<210> 135  
<211> 20

<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 135  
agcagagtga aataacaactt

20

<210> 136  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 136  
tgtcagctct acattaggca

20

<210> 137  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 137  
agtaagcccg gtctccctaag

20

<210> 138  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 138

aaatggaaaa ggacagcagc

20

<210> 139

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> control sequence

<400> 139

gctcagtggaa tatggatgag

20

<210> 140

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> control sequence

<400> 140

gctaaggcggtt caaggttgag

20

<210> 141

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> control sequence

<400> 141

gctcgggtggaa aatggatcag

20

<210> 142  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 142  
gggctttcat tagccacatt 20

<210> 143  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 143  
ggttggttca ctgcagtagt 20

<210> 144  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 144  
tgctcatgtt gtaatgttg 20

<210> 145  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 145  
gtcgaggaca gcgtcatacg 20

<210> 146  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 146  
cgacatccgc tcgtggtcca 20

<210> 147  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 147  
acatacggag tcatcatgaa 20

<210> 148  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 148

gcaatttctt catgaattct 20

<210> 149  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 149  
tcgtacccaaa cgtttatgtta 20

<210> 150  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 150  
cgccgaggct tccaggctgc 20

<210> 151  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 151  
ggcttagtcacctgcaacaac 20

<210> 152  
<211> 20

<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 152  
gcgtgcgtgcgtgcgtttcgct

20

<210> 153  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 153  
gctcagctgcgatacagaac

20

<210> 154  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 154  
agcgcgactagaaggtaagt

20

<210> 155  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>

<223> antisense sequence

<400> 155  
agggagacca aagtgcgagcg 20

<210> 156  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 156  
acatcttcaa attcttctag 20

<210> 157  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 157  
taggatattc tttcatgatc 20

<210> 158  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 158  
agaaggtagg acatttttc 20

<210> 159  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 159  
tttattccac tgatcaatat 20

<210> 160  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 160  
tcaataactt tattccactg 20

<210> 161  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 161  
ggttgcagtt tcttcatgaa 20

<210> 162  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<220>  
<221> modified\_base  
<222> 6  
<223> I

<400> 162  
tagganattc tttcatgatc

20

<210> 163  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<220>  
<221> modified\_base  
<222> 8  
<223> I

<400> 163  
ggttgcantt tcttcatgaa

20

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US98/16488

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :Please See Extra Sheet.

US CL :Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 91.1, 172.3, 320.1, 366, 375; 536/23.1, 23.2, 24.31, 24.5; 514/44

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

DIALOG, GENBANK, MEDLINE

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	SEIMIYA, H. et al. c-Jun NH2-Terminal Kinase-Mediated Activation of Interleukin-1-beta Converting Enzyme/CED-3-like Protease During Anticancer Drug-induced Apoptosis. J. Biological Chemistry. 14 February 1997, Vol. 272, pages 4631-4636, especially page 4632.	1-24
Y	GUPTA, S. et al. Selective Interaction of JNK Protein Kinase Isoforms With Transcription Factors. The EMBO Journal. 27 June 1996, Vol. 15, number 11, pages 2760-2770, especially page 2762.	1-24

 Further documents are listed in the continuation of Box C.  See patent family annex.

* Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
*A* document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
*B* earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
*L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
*O* document referring to an oral disclosure, use, exhibition or other means		
*P* document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search  
04 DECEMBER 1998

Date of mailing of the international search report

11 JAN 1999

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
Box PCT  
Washington, D.C. 20231  
Facsimile No. (703) 305-3230Authorized officer  
MARK SHIBUYA  
Telephone No. (703) 308-0196

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US98/16488

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	DERIJARD, B. et al. JNK1: A Protein Kinase Stimulated by UV Light and Ha-Ras That Binds and Phosphorylates the c-Jun Activation Domain. Cell. 25 March 1994, Vol. 76, pages 1025-1037, especially p. 1026, Figure 1.	1-24

**INTERNATIONAL SEARCH REPORT**

International application No.

PCT/US98/16488

**A. CLASSIFICATION OF SUBJECT MATTER:**  
IPC (6):

C12Q 1/68; C12P 19/34; C12N 15/63, 15/85; C12N 15/11; C07H 21/04; A61K 48/00

**A. CLASSIFICATION OF SUBJECT MATTER:**  
US CL :

435/6, 91.1, 172.3, 320.1, 366, 375; 536/23.1, 23.2, 24.31, 24.5; 514/44